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FILE 'HOME' ENTERED AT 09:49:57 ON 30 JUN 2004
=> file biosis,caba,caplus,embase,japio,lifesci,medline,scisearch,uspatfull
=> e jungblut peter/au
E1          344     JUNGBLUT P W/AU
E2            1     JUNGBLUT PAUL/AU
E3           71 --> JUNGBLUT PETER/AU
E4          118     JUNGBLUT PETER R/AU
E5            8     JUNGBLUT PETER ROMAN/AU
E6            1     JUNGBLUT PETER S/AU
E7           57     JUNGBLUT PETER W/AU
E8            2     JUNGBLUT PETER WILHELM/AU
E9          172     JUNGBLUT R/AU
E10         122     JUNGBLUT R M/AU
E11           1     JUNGBLUT R P/AU
E12           1     JUNGBLUT RALF/AU
=> s e1-e8 and mycobact?
L1           27 ("JUNGBLUT P W"/AU OR "JUNGBLUT PAUL"/AU OR "JUNGBLUT PETER"/AU
                OR "JUNGBLUT PETER R"/AU OR "JUNGBLUT PETER ROMAN"/AU OR "JUNGBL
                UT PETER S"/AU OR "JUNGBLUT PETER W"/AU OR "JUNGBLUT PETER WILHE
                LM"/AU) AND MYCOBACT?
=> dup rem l1
PROCESSING COMPLETED FOR L1
L2            16 DUP REM L1 (11 DUPLICATES REMOVED)
=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 16 ANSWERS - CONTINUE? Y/(N):y
 L2   ANSWER 1 OF 16  CAPLUS  COPYRIGHT 2004 ACS on STN DUPLICATE 1
AN   2004:414193  CAPLUS
TI   Web-accessible proteome databases for microbial research
AU   Pleissner, Klaus-Peter; Eifert, Till; Buettner, Sven; Schmidt, Frank;
     Boehme, Martina; Meyer, Thomas F.; Kaufmann, Stefan H. E.;   ***Jungblut,***
  ***     Peter R.***
CS   Max Planck Institute for Infection Biology, Berlin, Germany
SO   Proteomics (2004), 4(5), 1305-1313
     CODEN: PROTC7; ISSN: 1615-9853
PB   Wiley-VCH Verlag GmbH & Co. KGaA
DT   Journal
LA   English
AB   The anal. of proteomes of biol. organisms represents a major challenge of
     the post-genome era.  Classical proteomics combines two-dimensional
     electrophoresis (2-DE) and mass spectrometry (MS) for the identification
     of proteins.  Novel technologies such as isotope coded affinity tag
     (ICAT)-liq. chromatog./mass spectrometry (LC/MS) open new insights into
     protein alterations.  The vast amt. and diverse types of proteomic data
     require adequate web-accessible computational and database technologies
     for storage, integration, dissemination, anal. and visualization.  A
     proteome database system (http://www.mpiib-berlin.mpg.de/2D-PAGE) for
     microbial research has been constructed which integrates 2-DE/MS,
     ICAT-LC/MS and functional classification data of proteins with genomic,
     metabolic and other biol. knowledge sources.  The two-dimensional
     polyacrylamide gel electrophoresis database delivers exptl. data on
     microbial proteins including mass spectra for the validation of protein
     identification.  The ICAT-LC/MS database comprises exptl. data for protein
     alterations of   ***mycobacterial***   strains BCG vs. H37Rv.  By
     formulating complex queries within a functional protein classification
     database "FUNC_CLASS" for   ***Mycobacterium***   tuberculosis and
     Helicobacter pylori the researcher can gather precise information on
     genes, proteins, protein classes and metabolic pathways.  The use of the R
     language in the database architecture allows high-level data anal. and
     visualization to be performed "on-the-fly".  The database system is
     centrally administrated, and investigators without specific bioinformatic
     competence in database construction can submit their data.  The database
     system also serves as a template for a prototype of a European Proteome
     Database of Pathogenic Bacteria.  Currently, the database system includes
     proteome information for six strains of microorganisms.
RE.CNT  17    THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2   ANSWER 2 OF 16  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 2
AN   2004:150099  BIOSIS
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DN PREV200400154284
TI Complementary analysis of the ***Mycobacterium*** tuberculosis proteome by two-dimensional electrophoresis and isotope-coded affinity tag technology.
AU Schmidt, Frank; Donahoe, Samuel; Hagens, Kristine; Mattow, Jens; Schaible, Ulrich E.; Kaufmann, Stefan H. E.; Aebersold, Ruedi; ***Jungblut, Peter*** *** R.*** [Reprint Author]
CS Core Facility Protein Analysis, Max Planck Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Molecular & Cellular Proteomics, (January 2004) Vol. 3, No. 1, pp. 24-42. print.
ISSN: 1535-9476 (ISSN print).
DT Article
LA English
ED Entered STN: 17 Mar 2004
Last Updated on STN: 17 Mar 2004
AB Classical proteomics combined two-dimensional gel electrophoresis (2-DE) for the separation and quantification of proteins in a complex mixture with mass spectrometric identification of selected proteins. More recently, the combination of liquid chromatography (LC), stable isotope tagging, and tandem mass spectrometry (MS/MS) has emerged as an alternative quantitative proteomics technology. We have analyzed the proteome of ***Mycobacterium*** tuberculosis, a major human pathogen comprising about 4,000 genes, by (i) 2-DE and mass spectrometry (MS) and by (ii) the isotope-coded affinity tag (ICAT) reagent method and MS/MS. The data obtained by either technology were compared with respect to their selectivity for certain protein types and classes and with respect to the accuracy of quantification. Initial datasets of 60,000 peptide MS/MS spectra and 1,800 spots for the ICAT-LC/MS and 2-DE/MS methods, respectively, were reduced to 280 and 108 conclusively identified and quantified proteins, respectively. ICAT-LC/MS showed a clear bias for high Mr proteins and was complemented by the 2-DE/MS method, which showed a preference for low Mr proteins and also identified cysteine-free proteins that were transparent to the ICAT-LC/MS method. Relative quantification between two strains of the M. tuberculosis complex also revealed that the two technologies provide complementary quantitative information; whereas the ICAT-LC/MS method quantifies the sum of the protein species of one gene product, the 2-DE/MS method quantifies at the level of resolved protein species, including post-translationally modified and processed polypeptides. Our data indicate that different proteomic technologies applied to the same sample provide complementary types of information that contribute to a more complete understanding of the biological system studied.

L2 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:173461 CAPLUS
DN 138:220354
TI Vaccine against ***mycobacterial*** -induced diseases comprises Rv1511 protein or its functional epitope and chimeric protein
IN Grode, Leander; ***Jungblut, Peter R.*** ; Kaufmann, Stefan H. E.; Mattow, Jens; Mollenkopf, Hans-Joachim; Schaible, Ulrich
PA Max-Planck-Gesellschaft zur Foerderung der Wissenschaften E.V., Germany
SO PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003018053	A1	20030306	WO 2002-EP9345	20020821

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,

NE, SN, TD, TG
PRAI EP 2001-120194 A 20010822
AB The present invention relates to a pharmaceutical compn. comprising Rv1511 protein or nucleic acid encoding Rv1511 protein. Furthermore, the invention provides for pharmaceutical compns. comprising fusion proteins, polynucleotides, vector(s), host cell(s) or antibodies as described herein. In addn., the invention relates to recombinant (bacterial) host cells and methods for the prodn. of a vaccine. The vaccine is used for treating ***mycobacterial*** -induced diseases such as tuberculosis, tropical skin ulcer, ulceration, abscess, granulomatous skin disease, pulmonary disease, lymphadenitis, cutaneous and disseminated disease.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 16 USPATFULL on STN
AN 2003:257280 USPATFULL
TI Method for identifying helicobacter antigens
IN Meyer, Thomas F, Berlin, GERMANY, FEDERAL REPUBLIC OF
Jungblut, Peter , Berlin, GERMANY, FEDERAL REPUBLIC OF
Baumann, Dirk, Berlin, GERMANY, FEDERAL REPUBLIC OF
Aebischer, Anton, Berlin, GERMANY, FEDERAL REPUBLIC OF
Haas, Gaby, Berlin, GERMANY, FEDERAL REPUBLIC OF
Zimny-Arndt, Ursula, Berlin, GERMANY, FEDERAL REPUBLIC OF
Lamer, Stephanie, Berlin, GERMANY, FEDERAL REPUBLIC OF
Karaali, Galip, Berlin, GERMANY, FEDERAL REPUBLIC OF
Sabarth, Nicolas, Berlin, GERMANY, FEDERAL REPUBLIC OF
Wendland, Meike, Berlin, GERMANY, FEDERAL REPUBLIC OF
PI US 2003180330 A1 20030925
AI US 2003-257976 A1 20030429 (10)
WO 2001-EP4728 20010426
PRAI EP 2000-108968 20000427
EP 2001-101439 20010123
DT Utility
FS APPLICATION
LREP ROTHWELL, FIGG, ERNST & MANBECK, P.C., 1425 K STREET, N.W., SUITE 800, WASHINGTON, DC, 20005
CLMN Number of Claims: 38
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 3651
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to a method for characterizing or identifying proteins which are expressed by cultivated Helicobacter cells and which preferably react with human antisera. Thus, novel Helicobacter antigens are provided which are suitable as targets for the diagnostis, prevention or treatment of Helicobacter infections.

L2 ANSWER 5 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 2004:71856 BIOSIS
DN PREV200400073461
TI Comparative proteome analysis of culture supernatant proteins from virulent ***Mycobacterium*** tuberculosis H37Rv and attenuated M. bovis BCG Copenhagen.
AU Mattow, Jens [Reprint Author]; Schaible, Ulrich E.; Schmidt, Frank; Hagens, Kristine; Slejak, Frank; Brestrich, Gordon; Haeselbarth, Gisela; Mueller, Eva-Christina; ***Jungblut, Peter R.*** ; Kaufmann, Stefan H. E.
CS Department of Immunology, Max Planck Institute for Infection Biology, Schumannstr. 21-22, D-10117, Berlin, Germany
mattow@mpiib-berlin.mpg.de
SO Electrophoresis, (October 2003) Vol. 24, No. 19-20, pp. 3405-3420. print.
ISSN: 0173-0835 (ISSN print).
DT Article
LA English
ED Entered STN: 4 Feb 2004
Last Updated on STN: 4 Feb 2004
AB A comprehensive analysis of culture supernatant (CSN) proteins of ***Mycobacterium*** tuberculosis H37Rv was accomplished by combination of two-dimensional electrophoresis (2-DE), mass spectrometry, and N-terminal sequencing by Edman degradation. Analytical 2-DE gels resolved

approximately 1250 protein spots from CSN of M. tuberculosis H37Rv, 381 of which were identified by mass spectrometry and/or Edman degradation. This study revealed 137 different proteins, 42 of which had previously been described as secreted. Comparative proteome analysis of CSN from virulent M. tuberculosis H37Rv and attenuated ***Mycobacterium*** bovis BCG Copenhagen identified 39 M. tuberculosis-specific spots containing 27 different proteins, representing candidate antigens for novel vaccines and diagnostics in tuberculosis. These included five proteins encoded by open reading frames absent from M. bovis BCG, e.g., early secretory antigen target (Esat6), as well as 22 novel differential proteins, such as acetyl-CoA C-acetyltransferase (Rv0243) and two putative Esat6-like proteins (Rv1198, Rv1793).

L2 ANSWER 6 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
AN 2003:101214 CAPLUS
DN 139:288488
TI ***Mycobacterial*** proteomes
AU Mollenkopf, Hans-Joachim; Mattow, Jens; Schaible, Ulrich E.; Grode, Leander; Kaufmann, Stefan H. E.; ***Jungblut, Peter R.***
CS Department of Immunology, Max Planck Institute for Infection Biology, Berlin, D-10117, Germany
SO Methods in Enzymology (2002), 358(Bacterial Pathogenesis, Part C), 242-256
CODEN: MENZAU; ISSN: 0076-6879
PB Elsevier Science
DT Journal
LA English
AB The procedures for the two-dimensional gel electrophoresis for protein sepn. in combination with mass spectrometry (MS) for the identification and characterization of gel-sepd. proteins to systematically analyze the proteomes of different virulent and attenuated strains is described. The identification of ***Mycobacterium*** tuberculosis specific proteins is potential antigens for diagnosis of and vaccination against tuberculosis.

L2 ANSWER 7 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:23526 BIOSIS
DN PREV200300023526
TI The ***mycobacterial*** proteome database: An information base for biology and medicine.
AU ***Jungblut, Peter R.***
SO Tuberculosis (Edinburgh), (2002) Vol. 82, No. 2-3, pp. 145-146. print.
Meeting Info.: International Symposium on Current Developments in Drug Discovery for Tuberculosis. Bangalore, India. January 14-17, 2002.
ISSN: 1472-9792 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 1 Jan 2003
Last Updated on STN: 1 Jan 2003

L2 ANSWER 8 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:373593 BIOSIS
DN PREV200200373593
TI A European pathogenic microorganism proteome database: Construction and maintenance.
AU Pleissner, Klaus-Peter; Eifert, Till; ***Jungblut, Peter R.***
[Reprint author]
CS Core Facility Protein Analysis, Max Planck Institute for Infection Biology, Schumannstr. 20-21, D-10117, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Comparative and Functional Genomics, (April, 2002) Vol. 3, No. 2, pp. 97-100. print.
ISSN: 1531-6912.
DT Article
LA English
ED Entered STN: 3 Jul 2002
Last Updated on STN: 3 Jul 2002
AB A relational database structure based on MS-Access and MySQL to store and manage proteomics data was established. This system may be used to publish two-dimensional electrophoretic proteomics data, and also may be accessed by external users who want to compare their own data with those

in the databases. The maintenance of the database is managed centrally. The producers of proteomics data do not need to construct a database themselves. Users can introduce mass spectra into the database, which allows the searching of peptide mass fingerprints against their own protein sequence databases. The first release published in January 2002 contains data from ***Mycobacterium*** tuberculosis, Helicobacter pylori, Borrelia garinii, Francisella tularensis, Chlamydia pneumoniae, Mycoplasma pneumoniae, Jurkat T-cells and mouse mammary gland projects (http://www.mpiib-berlin.mpg.de/2D-PAGE/).

L2 ANSWER 9 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 5
AN 2001:440783 BIOSIS
DN PREV200100440783
TI Proteomics reveals open reading frames in ***Mycobacterium*** tuberculosis H37Rv not predicted by genomics.
AU ***Jungblut, Peter R.*** [Reprint author]; Mueller, Eva-Christina; Mattow, Jens; Kaufmann, Stefan H. E.
CS Core Facility for Protein Analysis, Max Planck Institute for Infection Biology, Schumannstr. 21-22, D-10117, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Infection and Immunity, (September, 2001) Vol. 69, No. 9, pp. 5905-5907. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 19 Sep 2001
Last Updated on STN: 22 Feb 2002
AB Genomics revealed the sequence of 3924 genes of the H37Rv strain of ***Mycobacterium*** tuberculosis. Proteomics complements genomics in showing which genes are really expressed, and here we show the expression of six genes not predicted by genomics, as proved by two-dimensional electrophoresis and matrix-assisted laser desorption ionization and nano-electrospray mass spectrometry.

L2 ANSWER 10 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 2001:472668 BIOSIS
DN PREV200100472668
TI Identification of proteins from ***Mycobacterium*** tuberculosis missing in attenuated ***Mycobacterium*** bovis BCG strains.
AU Mattow, Jens; ***Jungblut, Peter R.*** [Reprint author]; Schaible, Ulrich E.; Mollenkopf, Hans-Joachim; Lamer, Stephanie; Zimny-Arndt, Ursula; Hagens, Kristine; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS Central Support Unit Biochemistry, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Electrophoresis, (August, 2001) Vol. 22, No. 14, pp. 2936-2946. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 10 Oct 2001
Last Updated on STN: 23 Feb 2002
AB A proteome approach, combining high-resolution two-dimensional electrophoresis (2-DE) with mass spectrometry, was used to compare the cellular protein composition of two virulent strains of ***Mycobacterium*** tuberculosis with two attenuated strains of ***Mycobacterium*** bovis Bacillus Calmette-Guerin (BCG), in order to identify unique proteins of these strains. Emphasis was given to the identification of M. tuberculosis specific proteins, because we consider these proteins to represent putative virulence factors and interesting candidates for vaccination and diagnosis of tuberculosis. The genome of M. tuberculosis strain H37Rv comprises nearly 4000 predicted open reading frames. In contrast, the separation of proteins from whole ***mycobacterial*** cells by 2-DE resulted in silver-stained patterns comprising about 1800 distinct protein spots. Amongst these, 96 spots were exclusively detected either in the virulent (56 spots) or in the attenuated (40 spots) ***mycobacterial*** strains. Fifty-three of these spots were analyzed by mass spectrometry, of which 41 were identified, including 32 M. tuberculosis specific spots. Twelve M. tuberculosis specific spots were identified as proteins, encoded by genes

previously reported to be deleted in M. bovis BCG. The remaining 20 spots unique for M. tuberculosis were identified as proteins encoded by genes that are not known to be missing in M. bovis BCG.

L2 ANSWER 11 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7
AN 2001:378769 BIOSIS
DN PREV200100378769
TI Identification of acidic, low molecular mass proteins of ***Mycobacterium*** tuberculosis strain H37Rv by matrix-assisted laser desorption/ionization and electrospray ionization mass spectrometry.
AU Mattow, Jens [Reprint author]; ***Jungblut, Peter R.*** ; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
mattow@mpiib-berlin.mpg.de
SO Proteomics, (April, 2001) Vol. 1, No. 4, pp. 494-507. print.
ISSN: 1615-9853.
DT Article
LA English
ED Entered STN: 8 Aug 2001
Last Updated on STN: 19 Feb 2002
AB Matrix-assisted laser desorption/ionization-mass spectrometry peptide mass mapping and nano-electrospray ionization tandem mass spectrometry were used to identify acidic, low molecular mass proteins of ***Mycobacterium*** tuberculosis strain H37Rv. Proteins were extracted from whole cell lysates of ***mycobacteria*** , separated by high resolution two-dimensional electrophoresis (2-DE) and analysed by mass spectrometry (MS). Silver-stained 2-DE patterns resolved about 1800 distinct protein species, 190 of which had an observed isoelectric point and molecular mass in the range of pH 4 to 6 and 6 to 15 kDa, respectively. Seventy-six spots from this range were excised from Coomassie Brilliant Blue G250-stained gels and analysed by MS, from which 72 were identified. These spots were shown to represent products of as many as 50 different protein-coding genes. Ten genes gave rise to more than one protein species. Eleven spots contained more than one protein. The present study led to the identification of 15 ***mycobacterial*** proteins with assigned putative functions, 28 conserved hypothetical proteins and one unknown protein. Most proteins of the latter two groups had previously been predicted at the DNA level only. Six additional spots were shown to comprise proteins encoded by open reading frames that have not been predicted for M. tuberculosis H37Rv by genomic investigations.

L2 ANSWER 12 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:162940 BIOSIS
DN PREV200100162940
TI Matrix-assisted laser desorption-ionization mass spectrometry peptide mass fingerprinting for proteome analysis: Identification efficiency after on-blot or in-gel digestion with and without desalting procedures.
AU Lamer, Stephanie; ***Jungblut, Peter R.*** [Reprint author]
CS Central Support Unit Biochemistry, Max-Planck-Institute for Infection Biology, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Journal of Chromatography B, (10 March, 2001) Vol. 752, No. 2, pp. 311-322. print.
CODEN: JCBADL. ISSN: 0378-4347.
DT Article
LA English
ED Entered STN: 4 Apr 2001
Last Updated on STN: 15 Feb 2002
AB In theory, peptide mass fingerprinting by matrix assisted laser desorption-ionization mass spectrometry (MALDI-MS) has the potential to identify all of the proteins detected by silver staining on gels. In practice, if the genome of the organism investigated is completely sequenced, using current techniques, all proteins stained by Coomassie Brilliant Blue can be identified. This loss of identification sensitivity of ten to hundred-fold is caused by loss of peptides by surface contacts. Therefore, we performed digestion and transfer of peptides in the lower mul range and reduced the number of steps. The peptide mix obtained from in-gel or on-blot digestion was analyzed directly after digestion or after concentration on POROS R2 beads. Eight protein spots of a 2-DE gel from

Mycobacterium bovis BCG were identified using these four preparation procedures for MALDI-MS. Overall, on-blot digestion was as effective as in-gel digestion. Whereas higher signal intensities resulted after concentration, hydrophilic peptides are better detected by direct measurement of the peptide mix without POROS R2 concentration.

L2 ANSWER 13 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS
DN 133:149124
TI Identification of specific differentially expressed antigens
IN ***Jungblut, Peter*** ; Kaufmann, Stefan H. E.; Schaible, Ulrich; Mollenkopf, Hans; Raupach, Barbel; Zimny-Arndt, Ursula; Lamer, Stephanie; Mattow, Jens
PA Chiron Behring G.m.b.H. und Co., Germany
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000044392	A2	20000803	WO 2000-EP690	20000128
	WO 2000044392	A3	20001207		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1146889	A2	20011024	EP 2000-904979	20000128
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2002534994	T2	20021022	JP 2000-595694	20000128
PRAI	EP 1999-101590	A	19990129		
	WO 2000-EP690	W	20000128		

AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is differentially expressed in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L2 ANSWER 14 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8
AN 2000:227162 BIOSIS
DN PREV200000227162
TI Analysis of missed cleavage sites, tryptophan oxidation and N-terminal pyroglutamylation after in-gel tryptic digestion.
AU Thiede, Bernd [Reprint author]; Lamer, Stephanie; Mattow, Jens; Siejak, Frank; Dimmler, Christiane; Rudel, Thomas; ***Jungblut, Peter R.***
CS Max-Planck-Institut fuer Infektions-Biologie, Monbijoustrasse 2, D-10117, Berlin, Germany
SO Rapid Communications in Mass Spectrometry, (2000) Vol. 14, No. 6, pp. 496-502. print.
CODEN: RCMSEF. ISSN: 0951-4198.
DT Article
LA English
ED Entered STN: 7 Jun 2000
Last Updated on STN: 5 Jan 2002
AB Peptide mass fingerprinting is a powerful tool for the identification of

proteins. Trypsin is the most widely used enzyme for this purpose. Therefore, 104 protein digests from human Jurkat T cells and ***Mycobacterium*** were analyzed considering missed cleavage sites, tryptophan oxidation and N-terminal pyroglutamylation. About 90% of the matched peptides with missed cleavage sites could be classified into three groups: (i) lysine and arginine with a neighbouring proline on the carboxy-terminal side, (ii) neighboring lysines/arginines, and (iii) lysines and arginines with an aspartic acid or glutamic acid residue on either the amino- or carboxy-terminal side. The first group is already accounted for by search programs. The number of missed cleavage sites can be increased without reducing the precision of the database search by taking the other two groups into consideration. Peptides with tryptophan were observed in non, singly (+16 Da) and doubly (+32 Da) oxidized forms. The higher oxidized form was only observed with lower intensity in the presence of the lower oxidized form. Peptides with N-terminal glutamine were found always as pyroglutamate (-17 Da), and in the majority of cases in pairs with unmodified glutamine. These data can be used for the refinement of protein searches by peptide mass fingerprinting.

L2 ANSWER 15 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:546662 CAPLUS
DN 131:283488
TI The Dominance of Arginine-Containing Peptides in MALDI-Derived Tryptic Mass Fingerprints of Proteins
AU Krause, Eberhard; Wenschuh, Holger; ***Jungblut, Peter R.***
CS Institute of Molecular Pharmacology, Berlin, D-10315, Germany
SO Analytical Chemistry (1999), 71(19), 4160-4165
CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
AB Matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) is a powerful tool for mass fingerprinting of peptide mixts. obtained after enzymic in-gel digestion of proteins sepd. by two-dimensional electrophoresis (2-DE). In the course of a proteome anal. of ***mycobacteria*** using mass spectrometric identification, it was found that 94% of the most intense MALDI-MS peaks denote peptides bearing arginine at the C-terminal end. The effect was demonstrated to be equally prominent using an equimolar mixt. of the synthetic peptides known to be present in the tryptic digest of the ***mycobacterial*** 35 kDa antigen ("synthetic mass map"). In addn., several binary mixts. of synthetic peptides differing exclusively at the C terminus (Arg or Lys) were examd. to rationalize the higher sensitivity toward arginine-contg. peptides. The extent of the effect described depends on the matrix used and may facilitate a more reliable assignment of mass fingerprint data to protein sequences in databases.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 16 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 1999:432183 BIOSIS
DN PREV199900432183
TI A dynamic two-dimensional polyacrylamide gel electrophoresis database: The ***mycobacterial*** proteome via internet.
AU Mollenkopf, Hans-Joachim [Reprint author]; ***Jungblut, Peter Roman*** ; Raupach, Baerbel; Mattow, Jens; Lamer, Stephanie; Zimny-Arndt, Ursula; Schaible, Ulrich Emil; Kaufmann, Stefan Hugo Ernst
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Electrophoresis, (Aug., 1999) Vol. 20, No. 11, pp. 2172-2180. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB Proteome analysis by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry, in combination with protein chemical methods, is a powerful approach for the analysis of the protein composition of complex biological samples. Data organization is imperative for efficient handling of the vast amount of information

generated. Thus we have constructed a 2-D PAGE database to store and compare protein patterns of cell-associated and culture-supernatant proteins of different ***mycobacterial*** strains. In accordance with the guidelines for federated 2-DE databases, we developed a program that generates a dynamic 2-D PAGE database for the World-Wide-Web to organise and publish, via the internet, our results from proteome analysis of different ***Mycobacterium*** tuberculosis as well as ***Mycobacterium*** bovis BCG strains. The uniform resource locator for the database is http://www.mpiib-berlin.mpg.de/2D-PAGE and can be read with a Java compatible browser. The interactive hypertext markup language documents displayed are generated dynamically in each individual session from a rational data file, a 2-D gel image file and a map file describing the protein spots as polygons. The program consists of common gateway interface scripts written in PERL, minimizing the administrative workload of the database. Furthermore, the database facilitates not only interactive use, but also worldwide active participation of other scientific groups with their own data, requiring only minimal computer hardware and knowledge of information technology.

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=> e kaufmann stefan h e/au
E1            1     KAUFMANN STEFAN G/AU
E2            4     KAUFMANN STEFAN H/AU
E3          609 --> KAUFMANN STEFAN H E/AU
E4            1     KAUFMANN STEFAN H K/AU
E5            2     KAUFMANN STEFAN HUGO ERNST/AU
E6            1     KAUFMANN STEFAN J E/AU
E7            1     KAUFMANN STEFFEN/AU
E8            1     KAUFMANN STEMP D/AU
E9            8     KAUFMANN STEPHAN/AU
E10           1     KAUFMANN STEPHAN KH E/AU
E11          25     KAUFMANN STEPHEN/AU
E12           1     KAUFMANN STEPHEN A/AU

=> s e2-e5 and mycobact?
L3          236 ("KAUFMANN STEFAN H"/AU OR "KAUFMANN STEFAN H E"/AU OR "KAUFMANN
                 STEFAN H K"/AU OR "KAUFMANN STEFAN HUGO ERNST"/AU) AND MYCOBACT
                ?

=> s l3 and (differential? express?)
   3 FILES SEARCHED...
L4            2 L3 AND (DIFFERENTIAL? EXPRESS?)

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5             2 DUP REM L4 (0 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L5   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2000:535006  CAPLUS
DN   133:149124
TI   Identification of specific   ***differentially***     ***expressed***
     antigens
IN   Jungblut, Peter;   ***Kaufmann, Stefan H. E.***  ; Schaible, Ulrich;
     Mollenkopf, Hans; Raupach, Barbel; Zimny-Arndt, Ursula; Lamer, Stephanie;
     Mattow, Jens
PA   Chiron Behring G.m.b.H. und Co., Germany
SO   PCT Int. Appl., 110 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   WO 2000044392      A2   20000803       WO 2000-EP690    20000128
     WO 2000044392      A3   20001207
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
             CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
             IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
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MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1146889 A2 20011024 EP 2000-904979 20000128
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO
JP 2002534994 T2 20021022 JP 2000-595694 20000128
PRAI EP 1999-101590 A 19990129
WO 2000-EP690 W 20000128
AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is ***differentially*** ***expressed*** in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L5 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:330718 BIOSIS
DN PREV199900330718
TI Phenotypically activated gammadelta T lymphocytes in the peripheral blood of patients with tuberculosis.
AU Behr-Perst, Susanne I.; Munk, Martin E.; Schaberg, Tom; Ulrichs, Timo; Schulz, Ralf-Joachim; ***Kaufmann, Stefan H. E.*** [Reprint author]
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustrasse 2, 10117, Berlin, Germany
SO Journal of Infectious Diseases, (July, 1999) Vol. 180, No. 1, pp. 141-149. print.
CODEN: JIDIAQ. ISSN: 0022-1899.
DT Article
LA English
ED Entered STN: 24 Aug 1999
Last Updated on STN: 24 Aug 1999
AB Surface molecules with the potential relevance for resistance against ***Mycobacterium*** tuberculosis were investigated. The expression of lymphocyte function antigen-1, very late antigen (VLA)-4, L-selectin, intercellular adhesion molecule (ICAM)-1, major histocompatibility complex class II, Fas, and CD40 on alphabeta T cells, gammadelta T cells, NK cells, and monocytes of healthy donors and patients with tuberculosis were analyzed. A high activation status of gammadelta T cells and increased levels of soluble ICAM-1 in plasma of patients with tuberculosis versus healthy individuals was detected. Tuberculosis patients with and without an underlying systemic disease could be segregated by ***differential*** ***expression*** of VLA-4 and ICAM-1 on gammadelta T cells and on monocytes. The composition of peripheral blood mononuclear cells varied slightly, whereas the proportion of monocytes decreased significantly in patients with tuberculosis, compared with healthy controls. The activation phenotype of peripheral gammadelta T cells in patients with tuberculosis emphasizes the role of these T cells in controlling the inflammatory process during tuberculosis and perhaps other microbial infections.

=> e schaible ulrich/au
E1 1 SCHAIBLE ULLRICH E/AU
E2 1 SCHAIBLE ULRIC E/AU
E3 14 --> SCHAIBLE ULRICH/AU
E4 89 SCHAIBLE ULRICH E/AU
E5 2 SCHAIBLE ULRICH EMIL/AU
E6 9 SCHAIBLE ULRIKE/AU
E7 5 SCHAIBLE UWE/AU

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E8            1     SCHAIBLE UWE D/AU
E9            4     SCHAIBLE W/AU
E10           4     SCHAIBLE W L/AU
E11          10     SCHAIBLE WALTER/AU
E12           3     SCHAIBLE WOLFGANG/AU

=> s e1-e6 and mycobact?
L6           45 ("SCHAIBLE ULLRICH E"/AU OR "SCHAIBLE ULRIC E"/AU OR "SCHAIBLE
                ULRICH"/AU OR "SCHAIBLE ULRICH E"/AU OR "SCHAIBLE ULRICH EMIL"/A
                U OR "SCHAIBLE ULRIKE"/AU) AND MYCOBACT?

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7            27 DUP REM L6 (18 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 27 ANSWERS - CONTINUE? Y/(N):y

L7   ANSWER 1 OF 27     MEDLINE on STN
AN   2004286452      IN-PROCESS
DN   PubMed ID: 15186397
TI   Apoptosis paves the detour path for CD8 T cell activation against
     intracellular bacteria.
AU   Winau Florian; Kaufmann Stefan H E;   ***Schaible Ulrich E***
CS   Max-Planck-Institute for Infection Biology, Department of Immunology,
     Schumannstr. 21-22, D-10117 Berlin, Germany.
SO   Cellular microbiology, (2004 Jul) 6 (7) 599-607.
     Journal code: 100883691. ISSN: 1462-5814.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   IN-PROCESS; NONINDEXED; Priority Journals
ED   Entered STN: 20040610
     Last Updated on STN: 20040629
AB   Intracellular bacteria such as   ***Mycobacterium***   tuberculosis
     primarily infect macrophages.  Within these host cells, the pathogens are
     confined to phagosomes and their antigens are secluded from the classical
     MHC I presentation pathway.  Moreover, macrophages fail to express certain
     antigen presenting molecules like CD1 proteins.  As a result of this
     intracellular lifestyle, the pathways for the induction of MHC I- and
     CD1-restricted CD8 T cells by such microorganisms remain elusive.  Based
     on recent findings in tuberculosis and salmonellosis, we propose a new
     detour pathway for CD8 T cell activation against intracellular bacteria
     through apoptotic blebs from infected macrophages.  Pathogen-derived
     antigens including proteins and lipids are delivered from infected cells
     to non-infected dendritic cells.  Subsequently, these professional antigen
     presenting cells display microbial antigens through MHC I and CD1 to T
     cells.  Thus, cross-priming mediated by apoptotic vesicles is not just a
     matter of antigen distribution, but an intrinsic immunological function
     due to the nature of phagosomally located intracellular bacteria.  We
     consider infection-induced apoptosis the conditio sine qua non for
     antigen-specific CD8 T cell activation by phagosome-enclosed pathogens.
     This important new function of cell death in antibacterial immunity
     requires consideration for rational vaccine design.

L7   ANSWER 2 OF 27  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 1
AN   2004:165929  BIOSIS
DN   PREV200400167248
TI   Saposin C is required for lipid presentation by human CD1b.
AU   Winau, Florian; Schwierzeck, Vera; Hurwitz, Robert; Remmel, Natascha;
     Sieling, Peter A.; Modlin, Robert L.; Porcelli, Steven A.; Brinkmann,
     Volker; Sugita, Masahiko; Sandhoff, Konrad; Kaufmann, Stefan H. E.
     [Reprint Author];   ***Schaible, Ulrich E.***
CS   Department of Immunology, Max-Planck-Institute for Infection Biology,
     Schumannstrasse 21-22, D-10117, Berlin, Germany
     kaufmann@mpiib-berlin.mpg.de
SO   Nature Immunology, (February 2004) Vol. 5, No. 2, pp. 169-174. print.
     ISSN: 1529-2908 (ISSN print).
DT   Article
LA   English
```

ED Entered STN: 24 Mar 2004
Last Updated on STN: 24 Mar 2004
AB Lipids from ***Mycobacterium*** tuberculosis are presented through CD1 proteins to T lymphocytes in humans, but the accessory molecules required for antigen loading and presentation remain unidentified. Here we show that fibroblasts deficient in sphingolipid activator proteins (SAPs) transfected with CD1b failed to activate lipid-specific T cells. However, the T cell response was restored when fibroblasts were reconstituted with SAP-C but not other SAPs. Lipid antigen and SAP-C colocalized in lysosomal compartments, and liposome assays showed that SAP-C efficiently extracts antigen from membranes. Coprecipitation demonstrated direct molecular interaction between SAP-C and CD1b. We propose a model in which SAP-C exposes lipid antigens from intralysosomal membranes for loading onto CD1b. Thus, SAP-C represents a missing link in antigen presentation of lipids through CD1b to human T cells.

L7 ANSWER 3 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:452094 CAPLUS
TI "Menage a trois" against tuberculosis
AU Winau, Florian; ***Schaible, Ulrich E.***
CS Max-Planck-Institut fuer Infektionsbiologie, Berlin, D-10117, Germany
SO Bioforum (2004), 27(4), 62-63
CODEN: BFRME3; ISSN: 0940-0079
PB GIT Verlag GmbH & Co. KG
DT Journal; General Review
LA German
AB A review. The role of saposins was characterized in the recognition of lipid antigens of ***mycobacteria*** by T lymphocytes. The saposin protein SAP-C was able to ext. lipid antigens from artificial liposome membranes and to bind antigen-presenting CD1 proteins simultaneously. On the basis of this triangle relation, the antigens of ***Mycobacterium*** tuberculosis are recognized by the T cells.

L7 ANSWER 4 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 2004:150099 BIOSIS
DN PREV200400154284
TI Complementary analysis of the ***Mycobacterium*** tuberculosis proteome by two-dimensional electrophoresis and isotope-coded affinity tag technology.
AU Schmidt, Frank; Donahoe, Samuel; Hagens, Kristine; Mattow, Jens; ***Schaible, Ulrich E.*** ; Kaufmann, Stefan H. E.; Aebersold, Ruedi; Jungblut, Peter R. [Reprint Author]
CS Core Facility Protein Analysis, Max Planck Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Molecular & Cellular Proteomics, (January 2004) Vol. 3, No. 1, pp. 24-42. print.
ISSN: 1535-9476 (ISSN print).
DT Article
LA English
ED Entered STN: 17 Mar 2004
Last Updated on STN: 17 Mar 2004
AB Classical proteomics combined two-dimensional gel electrophoresis (2-DE) for the separation and quantification of proteins in a complex mixture with mass spectrometric identification of selected proteins. More recently, the combination of liquid chromatography (LC), stable isotope tagging, and tandem mass spectrometry (MS/MS) has emerged as an alternative quantitative proteomics technology. We have analyzed the proteome of ***Mycobacterium*** tuberculosis, a major human pathogen comprising about 4,000 genes, by (i) 2-DE and mass spectrometry (MS) and by (ii) the isotope-coded affinity tag (ICAT) reagent method and MS/MS. The data obtained by either technology were compared with respect to their selectivity for certain protein types and classes and with respect to the accuracy of quantification. Initial datasets of 60,000 peptide MS/MS spectra and 1,800 spots for the ICAT-LC/MS and 2-DE/MS methods, respectively, were reduced to 280 and 108 conclusively identified and quantified proteins, respectively. ICAT-LC/MS showed a clear bias for high Mr proteins and was complemented by the 2-DE/MS method, which showed a preference for low Mr proteins and also identified cysteine-free proteins that were transparent to the ICAT-LC/MS method. Relative

quantification between two strains of the M. tuberculosis complex also revealed that the two technologies provide complementary quantitative information; whereas the ICAT-LC/MS method quantifies the sum of the protein species of one gene product, the 2-DE/MS method quantifies at the level of resolved protein species, including post-translationally modified and processed polypeptides. Our data indicate that different proteomic technologies applied to the same sample provide complementary types of information that contribute to a more complete understanding of the biological system studied.

L7 ANSWER 5 OF 27 MEDLINE on STN
AN 2003009658 MEDLINE
DN PubMed ID: 12515808
TI A dangerous liaison between two major killers: ***Mycobacterium*** tuberculosis and HIV target dendritic cells through DC-SIGN.
CM Comment on: J Exp Med. 2003 Jan 6;197(1):121-7. PubMed ID: 12515819
Comment on: J Exp Med. 2003 Jan 6;197(1):7-17. PubMed ID: 12515809
AU Kaufmann Stefan H E; ***Schaible Ulrich E***
CS Department of Immunology, Max Planck Institute for Infection Biology, D-10117 Berlin, Germany.. kaufmann@mpiib-berlin.mpg.de
SO Journal of experimental medicine, (2003 Jan 6) 197 (1) 1-5.
Journal code: 2985109R. ISSN: 0022-1007.
CY United States
DT Commentary
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200302
ED Entered STN: 20030108
Last Updated on STN: 20030207
Entered Medline: 20030206

L7 ANSWER 6 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:173461 CAPLUS
DN 138:220354
TI Vaccine against ***mycobacterial*** -induced diseases comprises Rv1511 protein or its functional epitope and chimeric protein
IN Grode, Leander; Jungblut, Peter R.; Kaufmann, Stefan H. E.; Mattow, Jens; Mollenkopf, Hans-Joachim; ***Schaible, Ulrich***
PA Max-Planck-Gesellschaft zur Foerderung der Wissenschaften E.V., Germany
SO PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003018053	A1	20030306	WO 2002-EP9345	20020821

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI EP 2001-120194 A 20010822
AB The present invention relates to a pharmaceutical compn. comprising Rv1511 protein or nucleic acid encoding Rv1511 protein. Furthermore, the invention provides for pharmaceutical compns. comprising fusion proteins, polynucleotides, vector(s), host cell(s) or antibodies as described herein. In addn., the invention relates to recombinant (bacterial) host cells and methods for the prodn. of a vaccine. The vaccine is used for treating ***mycobacterial*** -induced diseases such as tuberculosis, tropical skin ulcer, ulceration, abscess, granulomatous skin disease, pulmonary disease, lymphadenitis, cutaneous and disseminated disease.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 2004:71856 BIOSIS
DN PREV200400073461
TI Comparative proteome analysis of culture supernatant proteins from virulent ***Mycobacterium*** tuberculosis H37Rv and attenuated M. bovis BCG Copenhagen.
AU Mattow, Jens [Reprint Author]; ***Schaible, Ulrich E.*** ; Schmidt, Frank; Hagens, Kristine; Slejak, Frank; Brestrich, Gordon; Haeselbarth, Gisela; Mueller, Eva-Christina; Jungblut, Peter R.; Kaufmann, Stefan H. E.
CS Department of Immunology, Max Planck Institute for Infection Biology, Schumannstr. 21-22, D-10117, Berlin, Germany
mattow@mpiib-berlin.mpg.de
SO Electrophoresis, (October 2003) Vol. 24, No. 19-20, pp. 3405-3420. print.
ISSN: 0173-0835 (ISSN print).
DT Article
LA English
ED Entered STN: 4 Feb 2004
Last Updated on STN: 4 Feb 2004
AB A comprehensive analysis of culture supernatant (CSN) proteins of ***Mycobacterium*** tuberculosis H37Rv was accomplished by combination of two-dimensional electrophoresis (2-DE), mass spectrometry, and N-terminal sequencing by Edman degradation. Analytical 2-DE gels resolved approximately 1250 protein spots from CSN of M. tuberculosis H37Rv, 381 of which were identified by mass spectrometry and/or Edman degradation. This study revealed 137 different proteins, 42 of which had previously been described as secreted. Comparative proteome analysis of CSN from virulent M. tuberculosis H37Rv and attenuated ***Mycobacterium*** bovis BCG Copenhagen identified 39 M. tuberculosis-specific spots containing 27 different proteins, representing candidate antigens for novel vaccines and diagnostics in tuberculosis. These included five proteins encoded by open reading frames absent from M. bovis BCG, e.g., early secretory antigen target (Esat6), as well as 22 novel differential proteins, such as acetyl-CoA C-acetyltransferase (Rv0243) and two putative Esat6-like proteins (Rv1198, Rv1793).

L7 ANSWER 8 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 2003:390344 BIOSIS
DN PREV200300390344
TI Apoptosis facilitates antigen presentation to T lymphocytes through MHC-I and CD1 in tuberculosis.
AU ***Schaible, Ulrich E.*** [Reprint Author]; Winau, Florian; Sieling, Peter A.; Fischer, Karsten; Collins, Helen L.; Hagens, Kristine; Modlin, Robert L.; Brinkmann, Volker; Kaufmann, Stefan H. E.
CS Department of Immunology, Max-Planck Institute for Infection Biology, Schumannstrasse 21-22, D-10117, Berlin, Germany
schaible@mpiib-berlin.mpg.de
SO Nature Medicine, (August 2003) Vol. 9, No. 8, pp. 1039-1046. print.
ISSN: 1078-8956 (ISSN print).
DT Article
LA English
ED Entered STN: 27 Aug 2003
Last Updated on STN: 27 Aug 2003
AB Protective immunity against ***Mycobacterium*** tuberculosis involves major histocompatibility complex class I (MHC-I)- and CD1-restricted CD8 T cells, but the mechanisms underlying antigen delivery to antigen-presenting molecules remain enigmatic. Macrophages, the primary host cells for ***mycobacteria*** , are CD1-negative. Here we show that M. tuberculosis phagosomes are secluded from the cytosolic MHC-I processing pathway and that ***mycobacteria*** -infected cells lose their antigen-presenting capacity. We also show that ***mycobacteria*** induce apoptosis in macrophages, causing the release of apoptotic vesicles that carry ***mycobacterial*** antigens to uninfected antigen-presenting cells (APCs). Inhibition of apoptosis reduced transfer of antigens to bystander cells and activation of CD8 T cells. Uninfected dendritic cells, which engulfed extracellular vesicles, were indispensable for subsequent cross-presentation of antigens, through MHC-I and CD1b, to T cells from ***mycobacteria*** -sensitized donors. This new 'detour' pathway for presentation of antigens from a phagosome-contained pathogen

shows the functional significance of infection-induced apoptosis in the activation of CD8 T cells specific for both protein and glycolipid antigens in tuberculosis.

L7 ANSWER 9 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 5
AN 2003:75308 BIOSIS
DN PREV200300075308
TI A dangerous liaison between two major killers: ***Mycobacterium*** tuberculosis and HIV target dendritic cells through DC-SIGN.
AU Kaufmann, Stefan H. E. [Reprint Author]; ***Schaible, Ulrich E.***
CS Department of Immunology, Max Planck Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
kaufmann@mpiib-berlin.mpg.de
SO Journal of Experimental Medicine, (January 6 2003) Vol. 197, No. 1, pp. 1-5. print.
ISSN: 0022-1007 (ISSN print).
DT Article
Editorial
LA English
ED Entered STN: 6 Feb 2003
Last Updated on STN: 6 Feb 2003

L7 ANSWER 10 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 2002:589940 BIOSIS
DN PREV200200589940
TI IL-4 and T cells are required for the generation of IgG1 isotype antibodies against cardiolipin.
AU Fischer, Karsten; Collins, Helen; Taniguchi, Masaru; Kaufmann, Stefan H. E.; ***Schaible, Ulrich E.*** [Reprint author]
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Schumannstrasse 20/21, 10117, Berlin, Germany
schaible@mpiib-berlin.mpg.de
SO Journal of Immunology, (March 15, 2002) Vol. 168, No. 6, pp. 2689-2694. print.
CODEN: JOIMA3. ISSN: 0022-1767.
DT Article
LA English
ED Entered STN: 13 Nov 2002
Last Updated on STN: 13 Nov 2002
AB Infection with ***Mycobacterium*** tuberculosis induces Abs against a vast array of ***mycobacterial*** lipids and glycolipids. One of the most prominent lipid Ags recognized is cardiolipin (CL). The kinetics of the generation of anti-CL Abs during infection reveals that IgM titers to CL increase over time. Interestingly, at day 30 postinfection CL-specific IgG1 appears, an isotype usually dependent on T cell help. Using an immunization schedule with CL/anti-CL Ab complexes, which induces antiphospholipid syndrome in mice, we show that the generation of IgG1 to CL requires IL-4 and that optimal production is T cell dependent. IgG1 production to CL was impaired in nude (nu/nu) mice devoid in conventional T cells, but was not affected in mice deficient for either alphabeta TCR+, gammadelta TCR+, CD4+, CD8+, or NK1.1+ T cells. We conclude that IgG1 production to CL depends on T cell help and IL-4, which can be provided by different T cell populations. This is the first report that IL-4 is indispensable for the induction of IgG1 Abs to lipid Ags.

L7 ANSWER 11 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7
AN 2003:19252 BIOSIS
DN PREV200300019252
TI Correction of the iron overload defect in beta-2-microglobulin knockout mice by lactoferrin abolishes their increased susceptibility to tuberculosis.
AU ***Schaible, Ulrich E.*** [Reprint Author]; Collins, Helen L.; Priem, Friedrich; Kaufmann, Stefan H. E.
CS Max-Planck-Institute for Infection Biology, Schumannstr. 21-22, D-10117, Berlin, Germany
schaible@mpiib-berlin.mpg.de
SO Journal of Experimental Medicine, (December 2 2002) Vol. 196, No. 11, pp. 1507-1513. print.

ISSN: 0022-1007 (ISSN print).
DT Article
LA English
ED Entered STN: 1 Jan 2003
Last Updated on STN: 1 Jan 2003
AB As a resident of early endosomal phagosomes, ***Mycobacterium*** tuberculosis is connected to the iron uptake system of the host macrophage. beta-2-microglobulin (beta2m) knockout (KO) mice are more susceptible to tuberculosis than wild-type mice, which is generally taken as a proof for the role of major histocompatibility complex class I (MHC-I)-restricted CD8 T cells in protection against M. tuberculosis. However, beta2m associates with a number of MHC-I-like proteins, including HFE. This protein regulates transferrin receptor mediated iron uptake and mutations in its gene cause hereditary iron overload (hemochromatosis). Accordingly, beta2m-deficient mice suffer from tissue iron overload. Here, we show that modulating the extracellular iron pool in beta2m-KO mice by lactoferrin treatment significantly reduces the burden of M. tuberculosis to numbers comparable to those observed in MHC class I-KO mice. In parallel, the generation of nitric oxide impaired in beta2m-KO mice was rescued. Conversely, iron overload in the immunocompetent host exacerbated disease. Consistent with this, iron deprivation in infected resting macrophages was detrimental for intracellular ***mycobacteria*** . Our data establish: (a) defective iron metabolism explains the increased susceptibility of beta2m-KO mice over MHC-I-KO mice, and (b) iron overload represents an exacerbating cofactor for tuberculosis.

L7 ANSWER 12 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:942005 CAPLUS
DN 138:121189
TI Vaccine development against tuberculosis
AU Kaufmann, Stefan H. E.; ***Schaible, Ulrich E.***
CS Max-Planck-Institut fuer Infektionsbiologie, Berlin, D-10117, Germany
SO BIOspektrum (2002), 8(5), 606, 608, 610-611
CODEN: BOSPFD; ISSN: 0947-0867
PB Spektrum Akademischer Verlag
DT Journal; General Review
LA German
AB A review on control of tuberculosis by the immune system, characterization of ***Mycobacterium*** tuberculosis, recognition of the intracellular tuberculosis pathogen by the immune system, and protection against ***mycobacteria*** by T cells. Development is discussed of 2 groups (cleavage vaccine, live virus vaccine) of new tuberculosis vaccines against tuberculosis of the lungs.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 8
AN 2003:101214 CAPLUS
DN 139:288488
TI ***Mycobacterial*** proteomes
AU Mollenkopf, Hans-Joachim; Mattow, Jens; ***Schaible, Ulrich E.*** ; Grode, Leander; Kaufmann, Stefan H. E.; Jungblut, Peter R.
CS Department of Immunology, Max Planck Institute for Infection Biology, Berlin, D-10117, Germany
SO Methods in Enzymology (2002), 358(Bacterial Pathogenesis, Part C), 242-256
CODEN: MENZAU; ISSN: 0076-6879
PB Elsevier Science
DT Journal
LA English
AB The procedures for the two-dimensional gel electrophoresis for protein sepn. in combination with mass spectrometry (MS) for the identification and characterization of gel-sepd. proteins to systematically analyze the proteomes of different virulent and attenuated strains is described. The identification of ***Mycobacterium*** tuberculosis specific proteins is potential antigens for diagnosis of and vaccination against tuberculosis.

L7 ANSWER 14 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 9
AN 2001:472668 BIOSIS
DN PREV200100472668

TI Identification of proteins from ***Mycobacterium*** tuberculosis missing in attenuated ***Mycobacterium*** bovis BCG strains.
AU Mattow, Jens; Jungblut, Peter R. [Reprint author]; ***Schaible, Ulrich*** *** E.*** ; Mollenkopf, Hans-Joachim; Lamer, Stephanie; Zimny-Arndt, Ursula; Hagens, Kristine; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS Central Support Unit Biochemistry, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Electrophoresis, (August, 2001) Vol. 22, No. 14, pp. 2936-2946. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 10 Oct 2001
Last Updated on STN: 23 Feb 2002
AB A proteome approach, combining high-resolution two-dimensional electrophoresis (2-DE) with mass spectrometry, was used to compare the cellular protein composition of two virulent strains of ***Mycobacterium*** tuberculosis with two attenuated strains of ***Mycobacterium*** bovis Bacillus Calmette-Guerin (BCG), in order to identify unique proteins of these strains. Emphasis was given to the identification of M. tuberculosis specific proteins, because we consider these proteins to represent putative virulence factors and interesting candidates for vaccination and diagnosis of tuberculosis. The genome of M. tuberculosis strain H37Rv comprises nearly 4000 predicted open reading frames. In contrast, the separation of proteins from whole ***mycobacterial*** cells by 2-DE resulted in silver-stained patterns comprising about 1800 distinct protein spots. Amongst these, 96 spots were exclusively detected either in the virulent (56 spots) or in the attenuated (40 spots) ***mycobacterial*** strains. Fifty-three of these spots were analyzed by mass spectrometry, of which 41 were identified, including 32 M. tuberculosis specific spots. Twelve M. tuberculosis specific spots were identified as proteins, encoded by genes previously reported to be deleted in M. bovis BCG. The remaining 20 spots unique for M. tuberculosis were identified as proteins encoded by genes that are not known to be missing in M. bovis BCG.

L7 ANSWER 15 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:593996 CAPLUS
DN 135:287418
TI ***Mycobacterial*** lysocardiolipin is exported from phagosomes upon cleavage of cardiolipin by a macrophage-derived lysosomal phospholipase A2
AU Fischer, Karsten; Chatterjee, Delphi; Torrelles, Jordi; Brennan, Patrick J.; Kaufmann, Stefan H. E.; ***Schaible, Ulrich E.***
CS Department of Immunology, Max-Planck Institute for Infection Biology, Berlin, 10117, Germany
SO Journal of Immunology (2001), 167(4), 2187-2192
CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB Pathogenic ***mycobacteria*** are able to survive and proliferate in phagosomes within host macrophages (M.phi.). This capability has been attributed in part to their cell wall, which consists of various unique lipids. Some of these are important in the host-pathogen interaction, such as resistance against microbicidal effector mechanisms and modulation of host cell functions, and/or are presented as Ags to T cells. Here the authors show that two lipids are released from the ***mycobacterial*** cell wall within the phagosome of infected M.phi. and transported out of this compartment into intracellular vesicles. One of these lipids was identified as lysocardiolipin. Lysocardiolipin was generated through cleavage of ***mycobacterial*** cardiolipin by a Ca2+-independent phospholipase A2 present in M.phi. lysosomes. This result indicates that lysosomal host cell enzymes can interact with released ***mycobacterial*** lipids to generate new products with a different intracellular distribution. This represents a novel pathway for the modification of bacterial lipid Ags.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 16 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS

DN 133:149124
TI Identification of specific differentially expressed antigens
IN Jungblut, Peter; Kaufmann, Stefan H. E.; ***Schaible, Ulrich*** ; Mollenkopf, Hans; Raupach, Barbel; Zimny-Arndt, Ursula; Lamer, Stephanie; Mattow, Jens
PA Chiron Behring G.m.b.H. und Co., Germany
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000044392	A2	20000803	WO 2000-EP690	20000128
	WO 2000044392	A3	20001207		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1146889	A2	20011024	EP 2000-904979	20000128
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2002534994	T2	20021022	JP 2000-595694	20000128
PRAI	EP 1999-101590	A	19990129		
	WO 2000-EP690	W	20000128		

AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is differentially expressed in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L7 ANSWER 17 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:291592 CAPLUS
DN 133:72809
TI Intersection of group I CD1 molecules and ***mycobacteria*** in different intracellular compartments of dendritic cells
AU ***Schaible, Ulrich E.*** ; Hagens, Kristine; Fischer, Karsten; Collins, Helen L.; Kaufmann, Stefan H. E.
CS Department of Immunology, Max Planck Institute for Infection Biology, Berlin, D-10117, Germany
SO Journal of Immunology (2000), 164(9), 4843-4852
CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB Human CD1a, CD1b, and CD1c mols. can present ***mycobacterial*** glycolipids to T cells. Because phagosomes contg. viable ***mycobacteria*** represent early endosomal compartments, the authors studied where ***mycobacterial*** glycolipids intersect with CD1 mols. in infected APC. CD1b and CD1c, but not CD1a, localized to late endosomes/lysosomes. CD1a and CD1c were predominantly expressed on the cell surface and in ***mycobacterial*** phagosomes of the early endosomal stage. In contrast, CD1b was present in a subset of ***mycobacterial*** phagosomes representing mature phagolysosomes. Released ***mycobacterial*** glycolipids including lipoarabinomannan and phosphatidylinositol mannosides were transported from the phagosome into late endosomes/lysosomes and to uninfected bystander cells. The

macrophage mannose receptor, which has been implicated in glycolipid uptake by APC for CD1b-mediated presentation, was absent from ***mycobacterial*** phagosomes and may therefore not be involved in trafficking of glycolipids between phagosomes and late endosomes/lysosomes. Thus, all 3 CD1 mols. have access to ***mycobacteria*** and glycolipids thereof, but at different intracellular sites. This allows sampling by CD1a, CD1b, and CD1c of ***mycobacterial*** glycolipids from different intracellular sites of the infected cell, which has important implications for processing and presentation of such antigens during ***mycobacterial*** infections.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 18 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:16296 CAPLUS
DN 135:165535
TI CD1 molecules and CD1-dependent T cells in bacterial infections: a link from innate to acquired immunity?
AU ***Schaible, Ulrich E.*** ; Kaufmann, Stefan H. E.
CS Max-Planck-Institute for Infection Biology, Berlin, Germany
SO Seminars in Immunology (2000), 12(6), 527-535
CODEN: SEIME2; ISSN: 1044-5323
PB Academic Press
DT Journal; General Review
LA English
AB A review with 78 refs. The MHC class I-like, non-polymorphic CD1 mols. represent a novel system for the presentation of glycolipid antigens to T lymphocytes. CD1-mediated T cell responses appear to play distinct roles during bacterial infections such as in tuberculosis. The authors deal here with 2 aspects of CD1-mediated immune reactions. First they discuss the role of group II CD1-dependent NK T cells in bacterial infection. Second, they provide an insight into differential intracellular meeting points for antigen processing between group I CD1 mols., ***mycobacteria*** , and ***mycobacterial*** glycolipid antigens.
(c) 2000 Academic Press.
RE.CNT 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 19 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2000:241448 BIOSIS
DN PREV200000241448
TI Isolation of RNA from ***mycobacteria*** grown under in vitro and in vivo conditions.
AU Dietrich, Guido [Reprint author]; ***Schaible, Ulrich E.*** ; Diehl, Klaus-Dieter; Mollenkopf, Hans-Joachim; Wiek, Sabine; Hess, Juergen; Hagens, Kristine; Kaufmann, Stefan H. E.; Knapp, Bernhard
CS Josef-Schneider-Str. 2, Institut fuer Hygiene und Mikrobiologie, University of Wuerzburg, D-97080, Wuerzburg, Germany
SO FEMS Microbiology Letters, (May 15, 2000) Vol. 186, No. 2, pp. 177-180. print.
CODEN: FMLED7. ISSN: 0378-1097.
DT Article
LA English
ED Entered STN: 14 Jun 2000
Last Updated on STN: 5 Jan 2002
AB Isolation of RNA from ***mycobacteria*** is very difficult to perform, and the yields are generally very low. We describe an approach to isolate RNA from ***mycobacterial*** species which combines the disruption of ***mycobacterial*** cells by a silica/ceramic matrix in a reciprocal shaker with the ease and efficiency of subsequent RNA purification on spin columns with silica gel-based membranes. This method is rapid, easy to perform and yields high amounts of pure, intact total RNA. Due to its safety, this method is applicable even to group 3 biological hazard organisms like ***Mycobacterium*** tuberculosis. By combining a method for the isolation of phagosomal bacteria from infected primary macrophages with the novel RNA isolation technique, we are able to monitor gene expression during infection even in bacteria which are rather resistant to genetic manipulation, like ***Mycobacterium*** bovis.

L7 ANSWER 20 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:510897 CAPLUS

DN 134:99221
TI Exploiting the immune system: toward new vaccines against intracellular bacteria
AU Hess, Jurgen; ***Schaible, Ulrich*** ; Raupach, Barbel; Kaufmann, Stefan H. E.
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Berlin, D-10117, Germany
SO Advances in Immunology (2000), 75, 1-88
CODEN: ADIMAV; ISSN: 0065-2776
PB Academic Press
DT Journal; General Review
LA English
AB A review with many refs. Studies on the development of new vaccines against intracellular bacteria by exploiting the host immune system are reviewed with many refs. Focus is on ***Mycobacterium*** tuberculosis, Salmonella spp. and Chlamydia spp. In addn., it is considered how intracellular bacteria can be used as vaccine carriers for heterologous antigens, particularly attenuated Salmonella and Listeria strains, as well as ***Mycobacterium*** bovis bacille Calmette Guerin (BCG). These strains not only represent suitable recombinant carriers for protein antigens but also are potential delivery systems for naked DNA constructs. (c) 2000 Academic Press.
RE.CNT 426 THERE ARE 426 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 21 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10
AN 1999:432183 BIOSIS
DN PREV199900432183
TI A dynamic two-dimensional polyacrylamide gel electrophoresis database: The ***mycobacterial*** proteome via internet.
AU Mollenkopf, Hans-Joachim [Reprint author]; Jungblut, Peter Roman; Raupach, Baerbel; Mattow, Jens; Lamer, Stephanie; Zimny-Arndt, Ursula; ***Schaible, Ulrich Emil*** ; Kaufmann, Stefan Hugo Ernst
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Electrophoresis, (Aug., 1999) Vol. 20, No. 11, pp. 2172-2180. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB Proteome analysis by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry, in combination with protein chemical methods, is a powerful approach for the analysis of the protein composition of complex biological samples. Data organization is imperative for efficient handling of the vast amount of information generated. Thus we have constructed a 2-D PAGE database to store and compare protein patterns of cell-associated and culture-supernatant proteins of different ***mycobacterial*** strains. In accordance with the guidelines for federated 2-DE databases, we developed a program that generates a dynamic 2-D PAGE database for the World-Wide-Web to organise and publish, via the internet, our results from proteome analysis of different ***Mycobacterium*** tuberculosis as well as ***Mycobacterium*** bovis BCG strains. The uniform resource locator for the database is http://www.mpiib-berlin.mpg.de/2D-PAGE and can be read with a Java compatible browser. The interactive hypertext markup language documents displayed are generated dynamically in each individual session from a rational data file, a 2-D gel image file and a map file describing the protein spots as polygons. The program consists of common gateway interface scripts written in PERL, minimizing the administrative workload of the database. Furthermore, the database facilitates not only interactive use, but also worldwide active participation of other scientific groups with their own data, requiring only minimal computer hardware and knowledge of information technology.

L7 ANSWER 22 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:747935 CAPLUS
DN 130:109010
TI Early IL-4 induction in bone marrow lymphoid precursor cells by ***mycobacterial*** lipoarabinomannan

AU Collins, Helen L.; ***Schaible, Ulrich E.*** ; Kaufmann, Stefan H. E.
CS Department of Immunology, Max Planck Institute for Infection Biology, Berlin, Germany
SO Journal of Immunology (1998), 161(10), 5546-5554
CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB IL-4 is produced promptly in response to certain infections and plays a key role in the Th1/Th2 T cell dichotomy; however, the cellular source remains a matter debate. Here we described the induction of IL-4 in bone marrow cells of normal and RAG-/- mice by both ***Mycobacterium*** tuberculosis and its major cell wall glycolipid, lipoarabinomannan. Characterization of the cell type responsible indicated that it was distinct from the NK1+ or CD4+ T cell previously ascribed the function of rapid IL-4 secretion. Cell-sorting expts. identified CD19+/B220+ precursor cells, presumably pre-B cells that produced IL-4 constitutively and whose frequency was rapidly and markedly up-regulated by lipoarabinomannan. Thus, pathogenic ***mycobacteria*** and their glycolipids may influence hemopoiesis by rapidly inducing IL-4 secretion in the bone marrow.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 23 OF 27 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:76718 CAPLUS
DN 128:166224
TI Cytokine activation leads to acidification and increases maturation of ***Mycobacterium*** avium-containing phagosomes in murine macrophages
AU ***Schaible, Ulrich E.*** ; Sturgill-Koszycki, Sheila; Schlesinger, Paul H.; Russell, David G.
CS Departments of Molecular Microbiology and Physiology and Cell Biology, Washington University, School of Medicine, St. Louis, MO, 63110, USA
SO Journal of Immunology (1998), 160(3), 1290-1296
CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB ***Mycobacterium*** avium (MAC) organisms multiply in phagosomes that have restricted fusigenicity with lysosomes, do not acidify due to a paucity of vacuolar proton-ATPases, yet remain accessible to recycling endosomes. During the course of ***mycobacterial*** infections, IFN-.gamma.-mediated activation of host and bystander macrophages is a key mechanism in the regulation of bacterial growth. Here the authors demonstrate that in keeping with earlier studies, cytokine activation of host macrophages leads to a decrease in MAC viability, demonstrable by bacterial esterase staining with fluorescein diacetate as well as colony-forming unit counts from infected cells. Anal. of the pH of MAC phagosomes demonstrated that the vacuoles in activated macrophages equilibrate to pH 5.2, in contrast to pH 6.3 in resting phagocytes. Biochem. anal. of MAC phagosomes from both resting and activated macrophages confirmed that the lower intraphagosomal pH correlated with an increased accumulation of proton-ATPases. Furthermore, the lower pH is reflected in the transition of MAC phagosomes to a point no longer accessible to transferrin, a marker of the recycling endosomal system. These alterations parallel the coalescence of bacterial vacuoles from individual bacilli in single vacuoles to communal vacuoles with multiple bacilli. These data demonstrate that bacteriostatic and bactericidal activities of activated macrophages are concomitant with alterations in the physiol. of the ***mycobacterial*** phagosome.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 24 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 11
AN 1998:6293 BIOSIS
DN PREV199800006293
TI Why intracellular parasitism need not be a degrading experience by ***Mycobacterium*** .
AU Russell, David G. [Reprint author]; Sturgill-Koszycki, Sheila; Vanheyningen, Tambryn; Collins, Helen; ***Schaible, Ulrich E.***

CS Dep. Molecular Microbiol., Washington Univ. Sch. Med., 660 South Euclid Ave., St. Louis, MO 63110, USA
SO Philosophical Transactions of the Royal Society of London B Biological Sciences, (Sept. 29, 1997) Vol. 352, No. 1359, pp. 1303-1310. print. ISSN: 0962-8436.
DT Article
LA English
ED Entered STN: 23 Dec 1997
Last Updated on STN: 23 Dec 1997
AB The success of ***mycobacteria*** as pathogens hinges on their ability to infect and persist within the macrophages of their host. However, activation of host macrophages by cytokines from a productive cellular immune response can stimulate the cells to kill their resident pathogens. This suggests that the interaction between host cell and microbe is in delicate balance, which can be tipped in favour of either organism. Biochemical analysis of ***mycobacterial*** vacuoles has shown them to be integral to the host cell's recycling endosomal system. As such they show limited acidification and hydrolytic activity despite possession of known lysosomal constituents such as cathepsins D, B and L, and LAMP 1. Even in established infections, they remain dynamic compartments accessible to several plasmalemma-derived constituents. Once the macrophage has been activated by IFN-gamma and TNF-alpha the vacuoles coalesce and acidify. This marks a distinct alteration in vacuole physiology and leads to stasis and death of the ***mycobacteria*** . ***Mycobacteria*** have developed several strategies to avoid this outcome. Most notably, live bacilli induce sustained release of IL-6 from infected macrophages. IL-6 blocks the ability of both polyclonal primary T cells and T-cell hybridomas to respond to appropriate stimuli. Such an activity could render the centres of infection foci, such as granulomas, anergic and thus avoid release of macrophage-activating cytokines. This paper discusses both the mechanisms by which ***mycobacteria*** try to ensure their success as intracellular pathogens and the relevance of these strategies to the overall understanding of ***mycobacterial*** diseases.

L7 ANSWER 25 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1998:107283 BIOSIS
DN PREV199800107283
TI Induction of early IL4 in bone marrow cells by ***mycobacterial*** lipoarabinomannan (LAM).
AU Collins, Helen; ***Schaible, Ulrich*** ; Kaufmann, Stefan H. E.
CS MPI Infection Biol., Monbijoustrasse 2, Berlin 10117, Germany
SO Immunology, (Dec., 1997) Vol. 92, No. SUPPL. 1, pp. 78. print.
Meeting Info.: 5th Annual Congress of the British Society for Immunology. Brighton, England, UK. December 2-5, 1997. British Society for Immunology.
CODEN: IMMUAM. ISSN: 0019-2805.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 3 Mar 1998
Last Updated on STN: 3 Mar 1998

L7 ANSWER 26 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 12
AN 1997:74114 BIOSIS
DN PREV199799380817
TI ***Mycobacterium*** -containing phagosomes are accessible to early endosomes and reflect a transitional state in normal phagosome biogenesis.
AU Sturgill-Koszycki, Sheila; ***Schaible, Ulrich E.*** ; Russell, David G. [Reprint author]
CS Dep. Molecular Microbiol., Washington Univ. Med. Sch., 660 S. Euclid Ave., St. Louis, MO 63110, USA
SO EMBO (European Molecular Biology Organization) Journal, (1996) Vol. 15, No. 24, pp. 6960-6968.
CODEN: EMJODG. ISSN: 0261-4189.
DT Article
LA English
ED Entered STN: 26 Feb 1997
Last Updated on STN: 26 Feb 1997
AB The success of ***Mycobacterium*** as a pathogen hinges on its ability to modulate its intracellular environment. ***Mycobacterium*** avium

reside in vacuoles with limited proteolytic activity, maintain cathepsin D in an immature form and remain accessible to internalized transferrin. Artificial acidification of isolated phagosomes facilitated processing of cathepsin D, demonstrating that pH alone limits proteolysis in these vacuoles. Moreover, analysis of IgG-bead phagosomes at early time points during their formation indicates that these phagosomes also acquire LAMP 1 and cathepsin D prior to the accumulation of proton-ATPases, and are transiently accessible to sorting endosomes. This suggests that the anomolous distribution of endosomal proteins in M. avium-containing vacuoles results from their arrested differentiation in an early transitional stage through which all phagosomes pass.

L7 ANSWER 27 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:96209 BIOSIS
DN PREV199799395412
TI The ***Mycobacterium*** avium vacuole represents an early stage in phagosome maturation.
AU Sturgill-Koszycki, Sheila; ***Schaible, Ulrich*** ; Russell, David G.
CS Dep. Molecular Microbiology, Washington Univ., St. Louis, MO, USA
SO Molecular Biology of the Cell, (1996) Vol. 7, No. SUPPL., pp. 327A.
Meeting Info.: Annual Meeting of the 6th International Congress on Cell Biology and the 36th American Society for Cell Biology. San Francisco, California, USA. December 7-11, 1996.
CODEN: MBCEEV. ISSN: 1059-1524.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 3 Mar 1997
Last Updated on STN: 3 Mar 1997

=> e mollenkopf hans/au
E1 68 MOLLENKOPF H J/AU
E2 1 MOLLENKOPF H J VVAYLO GENTSCHEV/AU
E3 22 --> MOLLENKOPF HANS/AU
E4 3 MOLLENKOPF HANS J/AU
E5 22 MOLLENKOPF HANS JOACHIM/AU
E6 1 MOLLENKOPF HEIDRUN/AU
E7 5 MOLLENKOPF HOWARD/AU
E8 1 MOLLENKOPF HOWARD C/AU
E9 1 MOLLENKOPF J/AU
E10 5 MOLLENKOPF J P/AU
E11 5 MOLLENKOPF J R/AU
E12 1 MOLLENKOPF JAMES D/AU

=> s e1-e5 and mycobact?
L8 50 ("MOLLENKOPF H J"/AU OR "MOLLENKOPF H J VVAYLO GENTSCHEV"/AU OR "MOLLENKOPF HANS"/AU OR "MOLLENKOPF HANS J"/AU OR "MOLLENKOPF HANS JOACHIM"/AU) AND MYCOBACT?

=> dup rem l8
PROCESSING COMPLETED FOR L8
L9 13 DUP REM L8 (37 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 13 ANSWERS - CONTINUE? Y/(N):y

L9 ANSWER 1 OF 13 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:173461 CAPLUS
DN 138:220354
TI Vaccine against ***mycobacterial*** -induced diseases comprises Rv1511 protein or its functional epitope and chimeric protein
IN Grode, Leander; Jungblut, Peter R.; Kaufmann, Stefan H. E.; Mattow, Jens; ***Mollenkopf, Hans-Joachim*** ; Schaible, Ulrich
PA Max-Planck-Gesellschaft zur Foerderung der Wissenschaften E.V., Germany
SO PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003018053	A1	20030306	WO 2002-EP9345	20020821

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI EP 2001-120194 A 20010822

AB The present invention relates to a pharmaceutical compn. comprising Rv1511 protein or nucleic acid encoding Rv1511 protein. Furthermore, the invention provides for pharmaceutical compns. comprising fusion proteins, polynucleotides, vector(s), host cell(s) or antibodies as described herein. In addn., the invention relates to recombinant (bacterial) host cells and methods for the prodn. of a vaccine. The vaccine is used for treating ***mycobacterial*** -induced diseases such as tuberculosis, tropical skin ulcer, ulceration, abscess, granulomatous skin disease, pulmonary disease, lymphadenitis, cutaneous and disseminated disease.

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1

AN 2003:536681 BIOSIS

DN PREV200300524305

TI Early granuloma formation after aerosol ***Mycobacterium*** tuberculosis infection is regulated by neutrophils via CXCR3-signaling chemokines.

AU Seiler, Peter [Reprint Author]; Aichele, Peter; Bandermann, Silke; Hauser, Anja E.; Lu, Bao; Gerard, Norma P.; Gerard, Craig; Ehlers, Stefan; ***Mollenkopf, Hans J.*** ; Kaufmann, Stefan H. E.

CS Department of Immunology, Max-Planck-Institut fuer Infektionsbiologie, Schumannstrasse 21/22, D-10117, Berlin, Germany
seiler@mpiib-berlin.mpg.de

SO European Journal of Immunology, (October 2003) Vol. 33, No. 10, pp. 2676-2686. print.
ISSN: 0014-2980 (ISSN print).

DT Article

LA English

ED Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003

AB Among the first cells to invade a site of infection, polymorphonuclear neutrophils (PMN) play an important role in the control of numerous infections. While PMN are considered critical for control of acute infections, their role in chronic infections remains less well understood. Here we report that PMN are essential for accurate early granuloma formation during chronic M. tuberculosis infection without influencing ***mycobacterial*** growth restriction. The PMN-mediated regulation of granuloma formation depended on chemokines signaling through CXCR3, in particular MIG, as indicated by immune histochemical analysis of lung sections from C57BL/6 wild-type and CXCR3-/- mutant mice and supported by microarray transcriptome analysis. Hence, PMN play a central role in regulating the focal granulomatous response in the lung, and this early granuloma formation can be segregated from long-term protection against pulmonary M. tuberculosis infection.

L9 ANSWER 3 OF 13 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2004:83284 CAPLUS

DN 140:234102

TI MAPPP: MHC class I antigenic peptide processing prediction

AU Hakenberg, Joerg; Nussbaum, Alexander K.; Schild, Hansjoerg; Rammensee, Hans-Georg; Kuttler, Christina; Holzhuetter, Hermann-Georg; Kloetzel, Peter-M.; Kaufmann, Stefan H. E.; ***Mollenkopf, Hans-Joachim***

CS Department of Theoretical Computer Science, University of Ulm, Ulm, Germany

SO Applied Bioinformatics (2003), 2(3), 155-158
CODEN: ABPIC8; ISSN: 1175-5636
PB Open Mind Journals
DT Journal
LA English
AB MAPPP is a bioinformatics tool for the prediction of potential antigenic epitopes presented on the cell surface by major histocompatibility complex class I (MHC I) mols. to CD8 pos. T lymphocytes. It combines existing predictions for proteasomal cleavage with peptide anchoring to MHC I mols.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 2002:390448 BIOSIS
DN PREV200200390448
TI Cultivation of ***Mycobacterium*** bovis BCG in bioreactors.
AU Dietrich, Guido [Reprint author]; ***Mollenkopf, Hans-Joachim*** ; Weber, Heinz; Knapp, Bernhard; Diehl, Klaus-Dieter; Hess, Juergen; Blackkolb, Friedrich; Broeker, Michael; Kaufmann, Stefan H. E.; Hundt, Erika
CS Bacterial Vaccine Research, Berna Biotech AG, Rehhagstr. 79, CH-3018, Berne, Switzerland
guido.dietrich@bernabiotech.com
SO Journal of Biotechnology, (3 July, 2002) Vol. 96, No. 3, pp. 259-270. print.
CODEN: JBITD4. ISSN: 0168-1656.
DT Article
LA English
ED Entered STN: 17 Jul 2002
Last Updated on STN: 17 Jul 2002
AB The ***Mycobacterium*** bovis BCG vaccine for commercial use is classically produced as surface pellicles by culture on synthetic medium. Under these conditions, reproducibility of the cultures and quality assessment are hampered by slow growth of the bacilli, the formation of bacterial aggregates and a high proportion of dead bacilli after processing and final formulation of the vaccine. Here, we established dispersed cultures of M. bovis BCG in synthetic media in small-scale bioreactors. These cultures allow recording and adjusting of culture parameters and give rise to single bacilli with a high degree of live bacteria. In the murine model, bioreactor-grown M. bovis BCG exhibited slightly stronger replication and persistence than the vaccine produced under the classical conditions. The protective efficacy against challenge with M. tuberculosis was identical for both vaccine preparations.

L9 ANSWER 5 OF 13 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
AN 2003:101214 CAPLUS
DN 139:288488
TI ***Mycobacterial*** proteomes
AU ***Mollenkopf, Hans-Joachim*** ; Mattow, Jens; Schaible, Ulrich E.; Grode, Leander; Kaufmann, Stefan H. E.; Jungblut, Peter R.
CS Department of Immunology, Max Planck Institute for Infection Biology, Berlin, D-10117, Germany
SO Methods in Enzymology (2002), 358(Bacterial Pathogenesis, Part C), 242-256
CODEN: MENZAU; ISSN: 0076-6879
PB Elsevier Science
DT Journal
LA English
AB The procedures for the two-dimensional gel electrophoresis for protein sepn. in combination with mass spectrometry (MS) for the identification and characterization of gel-sepd. proteins to systematically analyze the proteomes of different virulent and attenuated strains is described. The identification of ***Mycobacterium*** tuberculosis specific proteins is potential antigens for diagnosis of and vaccination against tuberculosis.

L9 ANSWER 6 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 2001:372848 BIOSIS
DN PREV200100372848
TI Protective efficacy against tuberculosis of ESAT-6 secreted by a live

Salmonella typhimurium vaccine carrier strain and expressed by naked DNA.
AU ***Mollenkopf, Hans-Joachim*** [Reprint author]; Groine-Triebkorn, Daniela; Andersen, Peter; Hess, Juergen; Kaufmann, Stefan H. E.
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, 10117, Berlin, Germany mollenkopf@mpiib-berlin.mpg.de
SO Vaccine, (16 July, 2001) Vol. 19, No. 28-29, pp. 4028-4035. print. CODEN: VACCDE. ISSN: 0264-410X.
DT Article
LA English
ED Entered STN: 8 Aug 2001
Last Updated on STN: 19 Feb 2002
AB We have constructed a recombinant (r) attenuated Salmonella typhimurium strain which secretes ESAT-6 of ***Mycobacterium*** tuberculosis via the hemolysin secretion system of E. coli. Additionally, we have ligated ESAT-6 to different commercially available mammalian expression systems for use as naked DNA vaccines. We studied protection against M. tuberculosis induced by vaccination with each of these constructs alone or in combination in mice. Vaccination with a single dose of r S. typhimurium secreting ESAT-6 reduced numbers of tubercle bacilli in the lungs throughout the course of infection. The combined prime-boost vaccination did not considerably enhance protection.

L9 ANSWER 7 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 5
AN 2001:472668 BIOSIS
DN PREV200100472668
TI Identification of proteins from ***Mycobacterium*** tuberculosis missing in attenuated ***Mycobacterium*** bovis BCG strains.
AU Mattow, Jens; Jungblut, Peter R. [Reprint author]; Schaible, Ulrich E.; ***Mollenkopf, Hans-Joachim*** ; Lamer, Stephanie; Zimny-Arndt, Ursula; Hagens, Kristine; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS Central Support Unit Biochemistry, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany jungblut@mpiib-berlin.mpg.de
SO Electrophoresis, (August, 2001) Vol. 22, No. 14, pp. 2936-2946. print. CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 10 Oct 2001
Last Updated on STN: 23 Feb 2002
AB A proteome approach, combining high-resolution two-dimensional electrophoresis (2-DE) with mass spectrometry, was used to compare the cellular protein composition of two virulent strains of ***Mycobacterium*** tuberculosis with two attenuated strains of ***Mycobacterium*** bovis Bacillus Calmette-Guerin (BCG), in order to identify unique proteins of these strains. Emphasis was given to the identification of M. tuberculosis specific proteins, because we consider these proteins to represent putative virulence factors and interesting candidates for vaccination and diagnosis of tuberculosis. The genome of M. tuberculosis strain H37Rv comprises nearly 4000 predicted open reading frames. In contrast, the separation of proteins from whole ***mycobacterial*** cells by 2-DE resulted in silver-stained patterns comprising about 1800 distinct protein spots. Amongst these, 96 spots were exclusively detected either in the virulent (56 spots) or in the attenuated (40 spots) ***mycobacterial*** strains. Fifty-three of these spots were analyzed by mass spectrometry, of which 41 were identified, including 32 M. tuberculosis specific spots. Twelve M. tuberculosis specific spots were identified as proteins, encoded by genes previously reported to be deleted in M. bovis BCG. The remaining 20 spots unique for M. tuberculosis were identified as proteins encoded by genes that are not known to be missing in M. bovis BCG.

L9 ANSWER 8 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 2001:340967 BIOSIS
DN PREV200100340967
TI Intracellular bacteria as targets and carriers for vaccination.
AU ***Mollenkopf, Hans*** [Reprint author]; Dietrich, Guido; Kaufmann, Stefan H. E.
CS Department of Immunology, Max-Planck-Institute for Infection Biology,

Schumannstr. 21/22, D-10117, Berlin, Germany
SO Biological Chemistry, (April, 2001) Vol. 382, No. 4, pp. 521-532. print.
ISSN: 1431-6730.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 18 Jul 2001
Last Updated on STN: 19 Feb 2002
AB In this review we discuss intracellular bacteria as targets and carriers for vaccines. For clarity and ease of comprehension, we focus on three microbes, ***Mycobacterium*** tuberculosis, Listeria monocytogenes and Salmonella, with an emphasis on tuberculosis, one of the leading causes of death from infectious disease. Novel vaccination strategies against these pathogens are currently being considered. One approach favors the use of live attenuated vaccines and vaccine carrier strains thereof, either for heterologous antigen presentation or DNA vaccine delivery. This strategy includes both the improvement of attenuated vaccine strains as well as the 'de novo' generation of attenuated variants of virulent pathogens. An alternative strategy relies on the application of subunit immunizations, either as nucleic acid vaccines or protein antigens of the pathogen. Finally, we present a short summary of the vaccination strategies against tuberculosis.

L9 ANSWER 9 OF 13 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS
DN 133:149124
TI Identification of specific differentially expressed antigens
IN Jungblut, Peter; Kaufmann, Stefan H. E.; Schaible, Ulrich; ***Mollenkopf, Hans*** ; Raupach, Barbel; Zimny-Arndt, Ursula; Lamer, Stephanie; Mattow, Jens
PA Chiron Behring G.m.b.H. und Co., Germany
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000044392	A2	20000803	WO 2000-EP690	20000128
	WO 2000044392	A3	20001207		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1146889	A2	20011024	EP 2000-904979	20000128
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2002534994	T2	20021022	JP 2000-595694	20000128
PRAI	EP 1999-101590	A	19990129		
	WO 2000-EP690	W	20000128		

AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is differentially expressed in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L9 ANSWER 10 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

DUPLICATE 7
AN 2000:241448 BIOSIS
DN PREV200000241448
TI Isolation of RNA from ***mycobacteria*** grown under in vitro and in vivo conditions.
AU Dietrich, Guido [Reprint author]; Schaible, Ulrich E.; Diehl, Klaus-Dieter; ***Mollenkopf, Hans-Joachim*** ; Wiek, Sabine; Hess, Juergen; Hagens, Kristine; Kaufmann, Stefan H. E.; Knapp, Bernhard
CS Josef-Schneider-Str. 2, Institut fuer Hygiene und Mikrobiologie, University of Wuerzburg, D-97080, Wuerzburg, Germany
SO FEMS Microbiology Letters, (May 15, 2000) Vol. 186, No. 2, pp. 177-180. print.
CODEN: FMLED7. ISSN: 0378-1097.
DT Article
LA English
ED Entered STN: 14 Jun 2000
Last Updated on STN: 5 Jan 2002
AB Isolation of RNA from ***mycobacteria*** is very difficult to perform, and the yields are generally very low. We describe an approach to isolate RNA from ***mycobacterial*** species which combines the disruption of ***mycobacterial*** cells by a silica/ceramic matrix in a reciprocal shaker with the ease and efficiency of subsequent RNA purification on spin columns with silica gel-based membranes. This method is rapid, easy to perform and yields high amounts of pure, intact total RNA. Due to its safety, this method is applicable even to group 3 biological hazard organisms like ***Mycobacterium*** tuberculosis. By combining a method for the isolation of phagosomal bacteria from infected primary macrophages with the novel RNA isolation technique, we are able to monitor gene expression during infection even in bacteria which are rather resistant to genetic manipulation, like ***Mycobacterium*** bovis.

L9 ANSWER 11 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8
AN 1999:432183 BIOSIS
DN PREV199900432183
TI A dynamic two-dimensional polyacrylamide gel electrophoresis database: The ***mycobacterial*** proteome via internet.
AU ***Mollenkopf, Hans-Joachim*** [Reprint author]; Jungblut, Peter Roman; Raupach, Baerbel; Mattow, Jens; Lamer, Stephanie; Zimny-Arndt, Ursula; Schaible, Ulrich Emil; Kaufmann, Stefan Hugo Ernst
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Electrophoresis, (Aug., 1999) Vol. 20, No. 11, pp. 2172-2180. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB Proteome analysis by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry, in combination with protein chemical methods, is a powerful approach for the analysis of the protein composition of complex biological samples. Data organization is imperative for efficient handling of the vast amount of information generated. Thus we have constructed a 2-D PAGE database to store and compare protein patterns of cell-associated and culture-supernatant proteins of different ***mycobacterial*** strains. In accordance with the guidelines for federated 2-DE databases, we developed a program that generates a dynamic 2-D PAGE database for the World-Wide-Web to organise and publish, via the internet, our results from proteome analysis of different ***Mycobacterium*** tuberculosis as well as ***Mycobacterium*** bovis BCG strains. The uniform resource locator for the database is http://www.mpiib-berlin.mpg.de/2D-PAGE and can be read with a Java compatible browser. The interactive hypertext markup language documents displayed are generated dynamically in each individual session from a rational data file, a 2-D gel image file and a map file describing the protein spots as polygons. The program consists of common gateway interface scripts written in PERL, minimizing the administrative workload of the database. Furthermore, the database facilitates not only interactive use, but also worldwide active participation of other scientific groups with their own data, requiring only minimal computer hardware and knowledge of information technology.

L9 ANSWER 12 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 1999:470696 BIOSIS
DN PREV199900470696
TI Comparative proteome analysis of ***Mycobacterium*** tuberculosis and ***Mycobacterium*** bovis BCG strains: Towards functional genomics of microbial pathogens.
AU Jungblut, P. R. [Reprint author]; Schaible, U. E.; ***Mollenkopf,*** H.-J.*** ; Zimny-Arndt, U.; Raupach, B.; Mattow, J.; Halada, P.; Lamer, S.; Hagens, K.; Kaufmann, S. H. E.
CS Protein Analysis Unit, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Molecular Microbiology, (Sept., 1999) Vol. 33, No. 6, pp. 1103-1117. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 9 Nov 1999
Last Updated on STN: 9 Nov 1999
AB In 1993, the WHO declared tuberculosis a global emergency on the basis that there are 8 million new cases per year. The complete genome of the strain H37Rv of the causative microorganism, ***Mycobacterium*** tuberculosis, comprising 3924 genes has been sequenced. We compared the proteomes of two non-virulent vaccine strains of M. bovis BCG (Chicago and Copenhagen) with two virulent strains of M. tuberculosis (H37Rv and Erdman) to identify protein candidates of value for the development of vaccines, diagnostics and therapeutics. The ***mycobacterial*** strains were analysed by two-dimensional electrophoresis (2-DE) combining non-equilibrium pH gradient electrophoresis (NEPHGE) with SDS-PAGE. Distinct and characteristic proteins were identified by mass spectrometry and introduced into a dynamic 2-DE database (http://www.mpiib-berlin.mpg.de/2D-PAGE). Silver-stained 2-DE patterns of ***mycobacterial*** cell proteins or culture supernatants contained 1800 or 800 spots, respectively, from which 263 wereidentified. Of these, 54 belong to the culture supernatant. Sixteen and 25 proteins differing in intensity or position between M. tuberculosis H37Rv and Erdman, and H37Rv and M. bovis BCG Chicago, respectively, were identified and categorized into protein classes. It is to be hoped that the availability of the ***mycobacterial*** proteome will facilitate the design of novel measures for prevention and therapy of one of the great health threats, tuberculosis.

L9 ANSWER 13 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10
AN 1999:60354 BIOSIS
DN PREV199900060354
TI Differential T cell responses to ***Mycobacterium*** tuberculosis ESAT6 in tuberculosis patients and healthy donors.
AU Ulrichs, Timo; Munk, Martin E. [Reprint author]; ***Mollenkopf, Hans*** ; Behr-Perst, Susanne; Colangeli, Roberto; Gennaro, Maria Laura; Kaufmann, Stefan H. E.
CS Max-Planck-Inst. Infection Biol., Monbijoustr. 2, D-10117 Berlin, Germany
SO European Journal of Immunology, (Dec., 1998) Vol. 28, No. 12, pp. 3949-3958. print.
CODEN: EJIMAF. ISSN: 0014-2980.
DT Article
LA English
ED Entered STN: 16 Feb 1999
Last Updated on STN: 16 Feb 1999
AB Vaccination against and diagnosis of tuberculosis are still insufficient. Proteins secreted by ***Mycobacterium*** tuberculosis induce strong immune responses in tuberculosis and constitute prime candidates for development of novel vaccines against tuberculosis as well as for immunodiagnostic assays. We investigated the role of the secreted proteins MPT63, MPT64 and ESAT6 from M. tuberculosis in healthy individuals and tuberculosis patients. None of the secreted proteins stimulated peripheral blood mononuclear cells from healthy donors. In contrast, CD4+ T cells from many tuberculosis patients were stimulated in an MHC class II-restricted fashion by ESAT6, but not by MPT63 or MPT64. T cell reactivities of tuberculosis patients were focused on the N-terminal

region of ESAT6. The ESAT6 T cell epitopes were presented by different HLA-DR phenotypes. Cell cultures responding to either ESAT6 or synthetic peptides thereof showed mRNA transcripts for macrophage inflammatory protein (MIP)-1 alpha, monocyte chemotactic protein (MCP)-1 or IL-8 and production of IFN-gamma and MIP1alpha. Our results suggest that the secreted M. tuberculosis proteins MPT63, MPT64 or ESAT6 do not stimulate unprimed T cells, and that ESAT6 may be a potential candidate antigen for detection of clinical disease.

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=> e raupach barbel/au
E1          95     RAUPACH B/AU
E2          22     RAUPACH BAERBEL/AU
E3          16 --> RAUPACH BARBEL/AU
E4           6     RAUPACH C/AU
E5          22     RAUPACH D C/AU
E6           2     RAUPACH D R/AU
E7           5     RAUPACH DALE C/AU
E8           1     RAUPACH DALE R/AU
E9           1     RAUPACH DIETMAR/AU
E10         17     RAUPACH E/AU
E11          1     RAUPACH E H FRIEDRICH/AU
E12        226     RAUPACH F/AU

=> s e1-e3 and mycobact?
L10         36 ("RAUPACH B"/AU OR "RAUPACH BAERBEL"/AU OR "RAUPACH BARBEL"/AU)
               AND MYCOBACT?

=> dup rem l10
PROCESSING COMPLETED FOR L10
L11           9 DUP REM L10 (27 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 9 ANSWERS - CONTINUE? Y/(N):y


L11  ANSWER 1 OF 9  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 1
AN   2003:18872  BIOSIS
DN   PREV200300018872
TI   Molecular basis of bacterial virulence and survival within infected hosts
     and the environment.
AU     ***Raupach, Baerbel***   [Reprint Author]; Reyrat, Jean-Marc
CS   Dept of Cellular Microbiology, Max Planck Institut fuer
     Infektionsbiologie, Schumannstrasse 21/22, Berlin, D-10117, Germany
     jmreyrat@pasteur.fr
SO   Trends in Microbiology, (December 2002) Vol. 10, No. 12, pp. 547-550.
     print.
     Meeting Info.: Molecular Basis of Bacterial Virulence and Survival within
     Infected Hosts and in the Environment. Spetsai, Greece. September 03-13,
     2002.
     ISSN: 0966-842X (ISSN print).
DT   Article
     Conference; (Meeting)
     Conference; Report; (Meeting Report)
LA   English
ED   Entered STN: 1 Jan 2003
     Last Updated on STN: 1 Jan 2003

L11  ANSWER 2 OF 9  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 2
AN   2001:326869  BIOSIS
DN   PREV200100326869
TI   MHC class Ia-restricted T cells partially account for beta2-microglobulin-
     dependent resistance to   ***Mycobacterium***   tuberculosis.
AU   Rolph, Michael S. [Reprint author];   ***Raupach, Baerbel***  ;
     Koebernick, Heidrun H. C.; Collins, Helen L.; Pararnau, Beatrice;
     Lemonnier, Francois A.; Kaufmann, Stefan H. E.
CS   Heart Research Institute, 145 Missenden Rd., Camperdown, Sydney, NSW,
     2050, Australia
     M.Rolph@hri.org.au
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SO European Journal of Immunology, (June, 2001) Vol. 31, No. 6, pp. 1944-1949. print.
CODEN: EJIMAF. ISSN: 0014-2980.
DT Article
LA English
ED Entered STN: 11 Jul 2001
Last Updated on STN: 19 Feb 2002
AB Recent studies have highlighted the heterogeneous nature of the CD8+ T cell response during human ***Mycobacterium*** tuberculosis infection; MHC class Ia, MHC class Ib and CD1 have all been identified as significant restriction elements. Here we have attempted to define the role of MHC class Ia in resistance to M. tuberculosis infection in mice. The course of M. tuberculosis infection in mice deficient in a single MHC class Ia molecule, either H2-Kb or H2-Db, was essentially identical to that observed in wild-type mice. In contrast, mice fully deficient in MHC class Ia molecules (H2-Kb/H2-Db double knockout mice) were substantially more susceptible to M. tuberculosis infection. However, the double knockout mice were not as susceptible as beta2-microglobulin-deficient mice, which have a broader phenotypic deficit. Thus, antigen presentation via MHC class Ia is an important component in resistance to M. tuberculosis, but its absence only partially accounts for the increased susceptibility of beta2-microglobulin-deficient mice.

L11 ANSWER 3 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 2002:302906 BIOSIS
DN PREV200200302906
TI Immune responses to intracellular bacteria.
AU ***Raupach, Baerbel*** [Reprint author]; Kaufmann, Stefan H. E. [Reprint author]
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Schumannstrasse 21-22, 10117, Berlin, Germany
Raupach@mpiib-berlin.mpg.de; Kaufmann@mpiib-berlin.mpg.de
SO Current Opinion in Immunology, (August, 2001) Vol. 13, No. 4, pp. 417-428. print.
CODEN: COPIEL. ISSN: 0952-7915.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 22 May 2002
Last Updated on STN: 22 May 2002

L11 ANSWER 4 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS
DN 133:149124
TI Identification of specific differentially expressed antigens
IN Jungblut, Peter; Kaufmann, Stefan H. E.; Schaible, Ulrich; Mollenkopf, Hans; ***Raupach, Barbel*** ; Zimny-Arndt, Ursula; Lamer, Stephanie; Mattow, Jens
PA Chiron Behring G.m.b.H. und Co., Germany
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000044392	A2	20000803	WO 2000-EP690	20000128
	WO 2000044392	A3	20001207		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1146889	A2	20011024	EP 2000-904979	20000128
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

JP 2002534994 T2 20021022 JP 2000-595694 20000128
PRAI EP 1999-101590 A 19990129
WO 2000-EP690 W 20000128
AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is differentially expressed in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L11 ANSWER 5 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 2000:181907 BIOSIS
DN PREV200000181907
TI Rapid neutrophil response controls fast-replicating intracellular bacteria but not slow-replicating ***Mycobacterium*** tuberculosis.
AU Seiler, Peter [Reprint author]; Aichele, Peter [Reprint author]; ***Raupach, Baerbel*** ; Odermatt, Bernhard; Steinhoff, Ulrich; Kaufmann, Stefan H.E.
CS Max-Planck-Institut fuer Infektionsbiologie, Monbijoustr. 2, D-10117, Berlin, Germany
SO Journal of Infectious Diseases, (Feb., 2000) Vol. 181, No. 2, pp. 671-680. print.
CODEN: JIDIAQ. ISSN: 0022-1899.
DT Article
LA English
ED Entered STN: 11 May 2000
Last Updated on STN: 4 Jan 2002
AB Being one of the first cells to invade the site of infection, neutrophils play an important role in the control of various bacterial and viral infections. In the present work, the contribution of neutrophils to the control of infection with different intracellular bacteria was investigated. Mice were treated with the neutrophil-depleting monoclonal antibody RB6-8C5, and the time course of infection in treated and untreated mice was compared by using intracellular bacterial species and strains varying in virulence and replication rate. The results indicate that neutrophils are crucial for the control of fast-replicating intracellular bacteria, whereas early neutrophil effector mechanisms are dispensable for the control of the slow-replicating ***Mycobacterium*** tuberculosis.

L11 ANSWER 6 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2000:468016 BIOSIS
DN PREV200000468016
TI Rapid neutrophil response controls fast-replicating intracellular bacteria but not ***Mycobacterium*** tuberculosis.
AU Seiler, P. [Reprint author]; Aichele, P. [Reprint author]; ***Raupach, B.*** [Reprint author]; Odermatt, B.; Steinhoff, U. [Reprint author]; Kaufmann, S. H. E. [Reprint author]
CS Max-Planck-Institut fuer Infektionsbiologie, Berlin, Germany
SO Immunology Letters, (September, 2000) Vol. 73, No. 2-3, pp. 145. print.
Meeting Info.: 24th European Immunology Meeting of the European Federation of Immunological Societies (EFIS). Poznan, Poland. September 23-26, 2000. European Federation of Immunological Societies.
CODEN: IMLED6. ISSN: 0165-2478.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 1 Nov 2000
Last Updated on STN: 10 Jan 2002

L11 ANSWER 7 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
AN 2000:510897 CAPLUS

DN 134:99221
TI Exploiting the immune system: toward new vaccines against intracellular bacteria
AU Hess, Jurgen; Schaible, Ulrich; ***Raupach, Barbel*** ; Kaufmann, Stefan H. E.
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Berlin, D-10117, Germany
SO Advances in Immunology (2000), 75, 1-88
CODEN: ADIMAV; ISSN: 0065-2776
PB Academic Press
DT Journal; General Review
LA English
AB A review with many refs. Studies on the development of new vaccines against intracellular bacteria by exploiting the host immune system are reviewed with many refs. Focus is on ***Mycobacterium*** tuberculosis, Salmonella spp. and Chlamydia spp. In addn., it is considered how intracellular bacteria can be used as vaccine carriers for heterologous antigens, particularly attenuated Salmonella and Listeria strains, as well as ***Mycobacterium*** bovis bacille Calmette Guerin (BCG). These strains not only represent suitable recombinant carriers for protein antigens but also are potential delivery systems for naked DNA constructs. (c) 2000 Academic Press.
RE.CNT 426 THERE ARE 426 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 1999:432183 BIOSIS
DN PREV199900432183
TI A dynamic two-dimensional polyacrylamide gel electrophoresis database: The ***mycobacterial*** proteome via internet.
AU Mollenkopf, Hans-Joachim [Reprint author]; Jungblut, Peter Roman; ***Raupach, Baerbel*** ; Mattow, Jens; Lamer, Stephanie; Zimny-Arndt, Ursula; Schaible, Ulrich Emil; Kaufmann, Stefan Hugo Ernst
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Electrophoresis, (Aug., 1999) Vol. 20, No. 11, pp. 2172-2180. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB Proteome analysis by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry, in combination with protein chemical methods, is a powerful approach for the analysis of the protein composition of complex biological samples. Data organization is imperative for efficient handling of the vast amount of information generated. Thus we have constructed a 2-D PAGE database to store and compare protein patterns of cell-associated and culture-supernatant proteins of different ***mycobacterial*** strains. In accordance with the guidelines for federated 2-DE databases, we developed a program that generates a dynamic 2-D PAGE database for the World-Wide-Web to organise and publish, via the internet, our results from proteome analysis of different ***Mycobacterium*** tuberculosis as well as ***Mycobacterium*** bovis BCG strains. The uniform resource locator for the database is http://www.mpiib-berlin.mpg.de/2D-PAGE and can be read with a Java compatible browser. The interactive hypertext markup language documents displayed are generated dynamically in each individual session from a rational data file, a 2-D gel image file and a map file describing the protein spots as polygons. The program consists of common gateway interface scripts written in PERL, minimizing the administrative workload of the database. Furthermore, the database facilitates not only interactive use, but also worldwide active participation of other scientific groups with their own data, requiring only minimal computer hardware and knowledge of information technology.

L11 ANSWER 9 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7
AN 1999:470696 BIOSIS
DN PREV199900470696
TI Comparative proteome analysis of ***Mycobacterium*** tuberculosis and

Mycobacterium bovis BCG strains: Towards functional genomics of microbial pathogens.

AU Jungblut, P. R. [Reprint author]; Schaible, U. E.; Mollenkopf, H.-J.; Zimny-Arndt, U.; ***Raupach, B.*** ; Mattow, J.; Halada, P.; Lamer, S.; Hagens, K.; Kaufmann, S. H. E.

CS Protein Analysis Unit, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany

SO Molecular Microbiology, (Sept., 1999) Vol. 33, No. 6, pp. 1103-1117. print.
CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 9 Nov 1999
Last Updated on STN: 9 Nov 1999

AB In 1993, the WHO declared tuberculosis a global emergency on the basis that there are 8 million new cases per year. The complete genome of the strain H37Rv of the causative microorganism, ***Mycobacterium*** tuberculosis, comprising 3924 genes has been sequenced. We compared the proteomes of two non-virulent vaccine strains of M. bovis BCG (Chicago and Copenhagen) with two virulent strains of M. tuberculosis (H37Rv and Erdman) to identify protein candidates of value for the development of vaccines, diagnostics and therapeutics. The ***mycobacterial*** strains were analysed by two-dimensional electrophoresis (2-DE) combining non-equilibrium pH gradient electrophoresis (NEPHGE) with SDS-PAGE. Distinct and characteristic proteins were identified by mass spectrometry and introduced into a dynamic 2-DE database (http://www.mpiib-berlin.mpg.de/2D-PAGE). Silver-stained 2-DE patterns of ***mycobacterial*** cell proteins or culture supernatants contained 1800 or 800 spots, respectively, from which 263 wereidentified. Of these, 54 belong to the culture supernatant. Sixteen and 25 proteins differing in intensity or position between M. tuberculosis H37Rv and Erdman, and H37Rv and M. bovis BCG Chicago, respectively, were identified and categorized into protein classes. It is to be hoped that the availability of the ***mycobacterial*** proteome will facilitate the design of novel measures for prevention and therapy of one of the great health threats, tuberculosis.

```
=> e zimny arndt ursula/au
E1           1     ZIMNY AMDT U/AU
E2          54     ZIMNY ARNDT U/AU
E3          36 --> ZIMNY ARNDT URSULA/AU
E4           3     ZIMNY ARNDT USCHI/AU
E5           7     ZIMNY B/AU
E6           2     ZIMNY B L/AU
E7           2     ZIMNY B U/AU
E8           3     ZIMNY BERND/AU
E9           1     ZIMNY BERND ULRICH/AU
E10          2     ZIMNY C/AU
E11          3     ZIMNY D/AU
E12          2     ZIMNY DIANA D/AU

=> s e1-e4 and mycobact?
L12         14 ("ZIMNY AMDT U"/AU OR "ZIMNY ARNDT U"/AU OR "ZIMNY ARNDT URSULA"
               /AU OR "ZIMNY ARNDT USCHI"/AU) AND MYCOBACT?

=> dup rem l12
PROCESSING COMPLETED FOR L12
L13           5 DUP REM L12 (9 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 5 ANSWERS - CONTINUE? Y/(N):y

L13  ANSWER 1 OF 5  USPATFULL on STN
AN     2003:257280  USPATFULL
TI     Method for identifying helicobacter antigens
IN     Meyer, Thomas F, Berlin, GERMANY, FEDERAL REPUBLIC OF
       Jungblut, Peter, Berlin, GERMANY, FEDERAL REPUBLIC OF
       Baumann, Dirk, Berlin, GERMANY, FEDERAL REPUBLIC OF
       Aebischer, Anton, Berlin, GERMANY, FEDERAL REPUBLIC OF
       Haas, Gaby, Berlin, GERMANY, FEDERAL REPUBLIC OF
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Zimny-Arndt, Ursula , Berlin, GERMANY, FEDERAL REPUBLIC OF
Lamer, Stephanie, Berlin, GERMANY, FEDERAL REPUBLIC OF
Karaali, Galip, Berlin, GERMANY, FEDERAL REPUBLIC OF
Sabarth, Nicolas, Berlin, GERMANY, FEDERAL REPUBLIC OF
Wendland, Meike, Berlin, GERMANY, FEDERAL REPUBLIC OF

PI US 2003180330 A1 20030925
AI US 2003-257976 A1 20030429 (10)
WO 2001-EP4728 20010426
PRAI EP 2000-108968 20000427
EP 2001-101439 20010123
DT Utility
FS APPLICATION
LREP ROTHWELL, FIGG, ERNST & MANBECK, P.C., 1425 K STREET, N.W., SUITE 800, WASHINGTON, DC, 20005
CLMN Number of Claims: 38
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 3651
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to a method for characterizing or identifying proteins which are expressed by cultivated Helicobacter cells and which preferably react with human antisera. Thus, novel Helicobacter antigens are provided which are suitable as targets for the diagnostis, prevention or treatment of Helicobacter infections.

L13 ANSWER 2 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 2001:472668 BIOSIS
DN PREV200100472668
TI Identification of proteins from ***Mycobacterium*** tuberculosis missing in attenuated ***Mycobacterium*** bovis BCG strains.
AU Mattow, Jens; Jungblut, Peter R. [Reprint author]; Schaible, Ulrich E.; Mollenkopf, Hans-Joachim; Lamer, Stephanie; ***Zimny-Arndt, Ursula*** ; Hagens, Kristine; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS Central Support Unit Biochemistry, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Electrophoresis, (August, 2001) Vol. 22, No. 14, pp. 2936-2946. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 10 Oct 2001
Last Updated on STN: 23 Feb 2002
AB A proteome approach, combining high-resolution two-dimensional electrophoresis (2-DE) with mass spectrometry, was used to compare the cellular protein composition of two virulent strains of ***Mycobacterium*** tuberculosis with two attenuated strains of ***Mycobacterium*** bovis Bacillus Calmette-Guerin (BCG), in order to identify unique proteins of these strains. Emphasis was given to the identification of M. tuberculosis specific proteins, because we consider these proteins to represent putative virulence factors and interesting candidates for vaccination and diagnosis of tuberculosis. The genome of M. tuberculosis strain H37Rv comprises nearly 4000 predicted open reading frames. In contrast, the separation of proteins from whole ***mycobacterial*** cells by 2-DE resulted in silver-stained patterns comprising about 1800 distinct protein spots. Amongst these, 96 spots were exclusively detected either in the virulent (56 spots) or in the attenuated (40 spots) ***mycobacterial*** strains. Fifty-three of these spots were analyzed by mass spectrometry, of which 41 were identified, including 32 M. tuberculosis specific spots. Twelve M. tuberculosis specific spots were identified as proteins, encoded by genes previously reported to be deleted in M. bovis BCG. The remaining 20 spots unique for M. tuberculosis were identified as proteins encoded by genes that are not known to be missing in M. bovis BCG.

L13 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS
DN 133:149124
TI Identification of specific differentially expressed antigens
IN Jungblut, Peter; Kaufmann, Stefan H. E.; Schaible, Ulrich; Mollenkopf, Hans; Raupach, Barbel; ***Zimny-Arndt, Ursula*** ; Lamer, Stephanie;

Mattow, Jens
PA Chiron Behring G.m.b.H. und Co., Germany
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000044392	A2	20000803	WO 2000-EP690	20000128
WO 2000044392	A3	20001207		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

EP 1146889	A2	20011024	EP 2000-904979	20000128
JP 2002534994	T2	20021022	JP 2000-595694	20000128
PRAI EP 1999-101590	A	19990129		
WO 2000-EP690	W	20000128		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is differentially expressed in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L13 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 1999:432183 BIOSIS
DN PREV199900432183
TI A dynamic two-dimensional polyacrylamide gel electrophoresis database: The ***mycobacterial*** proteome via internet.
AU Mollenkopf, Hans-Joachim [Reprint author]; Jungblut, Peter Roman; Raupach, Baerbel; Mattow, Jens; Lamer, Stephanie; ***Zimny-Arndt, Ursula*** ; Schaible, Ulrich Emil; Kaufmann, Stefan Hugo Ernst
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Electrophoresis, (Aug., 1999) Vol. 20, No. 11, pp. 2172-2180. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB Proteome analysis by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry, in combination with protein chemical methods, is a powerful approach for the analysis of the protein composition of complex biological samples. Data organization is imperative for efficient handling of the vast amount of information generated. Thus we have constructed a 2-D PAGE database to store and compare protein patterns of cell-associated and culture-supernatant proteins of different ***mycobacterial*** strains. In accordance with the guidelines for federated 2-DE databases, we developed a program that generates a dynamic 2-D PAGE database for the World-Wide-Web to organise and publish, via the internet, our results from proteome analysis of different ***Mycobacterium*** tuberculosis as well as ***Mycobacterium*** bovis BCG strains. The uniform resource locator for

the database is http://www.mpiib-berlin.mpg.de/2D-PAGE and can be read with a Java compatible browser. The interactive hypertext markup language documents displayed are generated dynamically in each individual session from a rational data file, a 2-D gel image file and a map file describing the protein spots as polygons. The program consists of common gateway interface scripts written in PERL, minimizing the administrative workload of the database. Furthermore, the database facilitates not only interactive use, but also worldwide active participation of other scientific groups with their own data, requiring only minimal computer hardware and knowledge of information technology.

L13 ANSWER 5 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 1999:470696 BIOSIS
DN PREV199900470696
TI Comparative proteome analysis of ***Mycobacterium*** tuberculosis and ***Mycobacterium*** bovis BCG strains: Towards functional genomics of microbial pathogens.
AU Jungblut, P. R. [Reprint author]; Schaible, U. E.; Mollenkopf, H.-J.; ***Zimny-Arndt, U.*** ; Raupach, B.; Mattow, J.; Halada, P.; Lamer, S.; Hagens, K.; Kaufmann, S. H. E.
CS Protein Analysis Unit, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Molecular Microbiology, (Sept., 1999) Vol. 33, No. 6, pp. 1103-1117. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 9 Nov 1999
Last Updated on STN: 9 Nov 1999
AB In 1993, the WHO declared tuberculosis a global emergency on the basis that there are 8 million new cases per year. The complete genome of the strain H37Rv of the causative microorganism, ***Mycobacterium*** tuberculosis, comprising 3924 genes has been sequenced. We compared the proteomes of two non-virulent vaccine strains of M. bovis BCG (Chicago and Copenhagen) with two virulent strains of M. tuberculosis (H37Rv and Erdman) to identify protein candidates of value for the development of vaccines, diagnostics and therapeutics. The ***mycobacterial*** strains were analysed by two-dimensional electrophoresis (2-DE) combining non-equilibrium pH gradient electrophoresis (NEPHGE) with SDS-PAGE. Distinct and characteristic proteins were identified by mass spectrometry and introduced into a dynamic 2-DE database (http://www.mpiib-berlin.mpg.de/2D-PAGE). Silver-stained 2-DE patterns of ***mycobacterial*** cell proteins or culture supernatants contained 1800 or 800 spots, respectively, from which 263 wereidentified. Of these, 54 belong to the culture supernatant. Sixteen and 25 proteins differing in intensity or position between M. tuberculosis H37Rv and Erdman, and H37Rv and M. bovis BCG Chicago, respectively, were identified and categorized into protein classes. It is to be hoped that the availability of the ***mycobacterial*** proteome will facilitate the design of novel measures for prevention and therapy of one of the great health threats, tuberculosis.

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=> e lamer stephanie/au
E1          93     LAMER S/AU
E2           6     LAMER STEFANIE/AU
E3          33 --> LAMER STEPHANIE/AU
E4           5     LAMER SYLVIE/AU
E5          22     LAMER T/AU
E6           1     LAMER T C/AU
E7          48     LAMER T J/AU
E8           4     LAMER THIERRY/AU
E9           6     LAMER TIM J/AU
E10          1     LAMER TIMOTHY J/AU
E11          1     LAMER V/AU
E12         18     LAMER V K/AU

=> s e1-e3 and mycobact?
L14         27 ("LAMER S"/AU OR "LAMER STEFANIE"/AU OR "LAMER STEPHANIE"/AU)
               AND MYCOBACT?
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=> dup rem l14
PROCESSING COMPLETED FOR L14
L15            7 DUP REM L14 (20 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 7 ANSWERS - CONTINUE? Y/(N):y


L15  ANSWER 1 OF 7  USPATFULL on STN
AN      2003:257280  USPATFULL
TI      Method for identifying helicobacter antigens
IN      Meyer, Thomas F, Berlin, GERMANY, FEDERAL REPUBLIC OF
        Jungblut, Peter, Berlin, GERMANY, FEDERAL REPUBLIC OF
        Baumann, Dirk, Berlin, GERMANY, FEDERAL REPUBLIC OF
        Aebischer, Anton, Berlin, GERMANY, FEDERAL REPUBLIC OF
        Haas, Gaby, Berlin, GERMANY, FEDERAL REPUBLIC OF
        Zimny-Arndt, Ursula, Berlin, GERMANY, FEDERAL REPUBLIC OF
            ***Lamer, Stephanie***  , Berlin, GERMANY, FEDERAL REPUBLIC OF
        Karaali, Galip, Berlin, GERMANY, FEDERAL REPUBLIC OF
        Sabarth, Nicolas, Berlin, GERMANY, FEDERAL REPUBLIC OF
        Wendland, Meike, Berlin, GERMANY, FEDERAL REPUBLIC OF
PI      US 2003180330       A1   20030925
AI      US 2003-257976      A1   20030429 (10)
        WO 2001-EP4728           20010426
PRAI    EP 2000-108968       20000427
        EP 2001-101439       20010123
DT      Utility
FS      APPLICATION
LREP    ROTHWELL, FIGG, ERNST & MANBECK, P.C., 1425 K STREET, N.W., SUITE 800,
        WASHINGTON, DC, 20005
CLMN    Number of Claims: 38
ECL     Exemplary Claim: 1
DRWN    23 Drawing Page(s)
LN.CNT 3651
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB      The present invention relates to a method for characterizing or
        identifying proteins which are expressed by cultivated Helicobacter
        cells and which preferably react with human antisera. Thus, novel
        Helicobacter antigens are provided which are suitable as targets for the
        diagnostis, prevention or treatment of Helicobacter infections.

L15  ANSWER 2 OF 7  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 1
AN   2001:472668  BIOSIS
DN   PREV200100472668
TI   Identification of proteins from  ***Mycobacterium***  tuberculosis
     missing in attenuated  ***Mycobacterium***  bovis BCG strains.
AU   Mattow, Jens; Jungblut, Peter R. [Reprint author]; Schaible, Ulrich E.;
     Mollenkopf, Hans-Joachim;  ***Lamer, Stephanie***  ; Zimny-Arndt, Ursula;
     Hagens, Kristine; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS   Central Support Unit Biochemistry, Max-Planck-Institute for Infection
     Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
     jungblut@mpiib-berlin.mpg.de
SO   Electrophoresis, (August, 2001) Vol. 22, No. 14, pp. 2936-2946. print.
     CODEN: ELCTDN. ISSN: 0173-0835.
DT   Article
LA   English
ED   Entered STN: 10 Oct 2001
     Last Updated on STN: 23 Feb 2002
AB   A proteome approach, combining high-resolution two-dimensional
     electrophoresis (2-DE) with mass spectrometry, was used to compare the
     cellular protein composition of two virulent strains of
       ***Mycobacterium***  tuberculosis with two attenuated strains of
       ***Mycobacterium***  bovis Bacillus Calmette-Guerin (BCG), in order to
     identify unique proteins of these strains. Emphasis was given to the
     identification of M. tuberculosis specific proteins, because we consider
     these proteins to represent putative virulence factors and interesting
     candidates for vaccination and diagnosis of tuberculosis. The genome of
     M. tuberculosis strain H37Rv comprises nearly 4000 predicted open reading
     frames. In contrast, the separation of proteins from whole
```

mycobacterial cells by 2-DE resulted in silver-stained patterns comprising about 1800 distinct protein spots. Amongst these, 96 spots were exclusively detected either in the virulent (56 spots) or in the attenuated (40 spots) ***mycobacterial*** strains. Fifty-three of these spots were analyzed by mass spectrometry, of which 41 were identified, including 32 M. tuberculosis specific spots. Twelve M. tuberculosis specific spots were identified as proteins, encoded by genes previously reported to be deleted in M. bovis BCG. The remaining 20 spots unique for M. tuberculosis were identified as proteins encoded by genes that are not known to be missing in M. bovis BCG.

L15 ANSWER 3 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 2001:162940 BIOSIS
DN PREV200100162940
TI Matrix-assisted laser desorption-ionization mass spectrometry peptide mass fingerprinting for proteome analysis: Identification efficiency after on-blot or in-gel digestion with and without desalting procedures.
AU ***Lamer, Stephanie*** ; Jungblut, Peter R. [Reprint author]
CS Central Support Unit Biochemistry, Max-Planck-Institute for Infection Biology, Berlin, Germany
jungblut@mpiib-berlin.mpg.de
SO Journal of Chromatography B, (10 March, 2001) Vol. 752, No. 2, pp. 311-322. print.
CODEN: JCBADL. ISSN: 0378-4347.
DT Article
LA English
ED Entered STN: 4 Apr 2001
Last Updated on STN: 15 Feb 2002
AB In theory, peptide mass fingerprinting by matrix assisted laser desorption-ionization mass spectrometry (MALDI-MS) has the potential to identify all of the proteins detected by silver staining on gels. In practice, if the genome of the organism investigated is completely sequenced, using current techniques, all proteins stained by Coomassie Brilliant Blue can be identified. This loss of identification sensitivity of ten to hundred-fold is caused by loss of peptides by surface contacts. Therefore, we performed digestion and transfer of peptides in the lower mul range and reduced the number of steps. The peptide mix obtained from in-gel or on-blot digestion was analyzed directly after digestion or after concentration on POROS R2 beads. Eight protein spots of a 2-DE gel from ***Mycobacterium*** bovis BCG were identified using these four preparation procedures for MALDI-MS. Overall, on-blot digestion was as effective as in-gel digestion. Whereas higher signal intensities resulted after concentration, hydrophilic peptides are better detected by direct measurement of the peptide mix without POROS R2 concentration.

L15 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS
DN 133:149124
TI Identification of specific differentially expressed antigens
IN Jungblut, Peter; Kaufmann, Stefan H. E.; Schaible, Ulrich; Mollenkopf, Hans; Raupach, Barbel; Zimny-Arndt, Ursula; ***Lamer, Stephanie*** ; Mattow, Jens
PA Chiron Behring G.m.b.H. und Co., Germany
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000044392	A2	20000803	WO 2000-EP690	20000128
	WO 2000044392	A3	20001207		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,

CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1146889 A2 20011024 EP 2000-904979 20000128
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
JP 2002534994 T2 20021022 JP 2000-595694 20000128
PRAI EP 1999-101590 A 19990129
WO 2000-EP690 W 20000128
AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is differentially expressed in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L15 ANSWER 5 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 2000:227162 BIOSIS
DN PREV200000227162
TI Analysis of missed cleavage sites, tryptophan oxidation and N-terminal pyroglutamylation after in-gel tryptic digestion.
AU Thiede, Bernd [Reprint author]; ***Lamer, Stephanie*** ; Mattow, Jens; Siejak, Frank; Dimmler, Christiane; Rudel, Thomas; Jungblut, Peter R.
CS Max-Planck-Institut fuer Infektions-Biologie, Monbijoustrasse 2, D-10117, Berlin, Germany
SO Rapid Communications in Mass Spectrometry, (2000) Vol. 14, No. 6, pp. 496-502. print.
CODEN: RCMSEF. ISSN: 0951-4198.
DT Article
LA English
ED Entered STN: 7 Jun 2000
Last Updated on STN: 5 Jan 2002
AB Peptide mass fingerprinting is a powerful tool for the identification of proteins. Trypsin is the most widely used enzyme for this purpose. Therefore, 104 protein digests from human Jurkat T cells and ***Mycobacterium*** were analyzed considering missed cleavage sites, tryptophan oxidation and N-terminal pyroglutamylation. About 90% of the matched peptides with missed cleavage sites could be classified into three groups: (i) lysine and arginine with a neighbouring proline on the carboxy-terminal side, (ii) neighboring lysines/arginines, and (iii) lysines and arginines with an aspartic acid or glutamic acid residue on either the amino- or carboxy-terminal side. The first group is already accounted for by search programs. The number of missed cleavage sites can be increased without reducing the precision of the database search by taking the other two groups into consideration. Peptides with tryptophan were observed in non, singly (+16 Da) and doubly (+32 Da) oxidized forms. The higher oxidized form was only observed with lower intensity in the presence of the lower oxidized form. Peptides with N-terminal glutamine were found always as pyroglutamate (-17 Da), and in the majority of cases in pairs with unmodified glutamine. These data can be used for the refinement of protein searches by peptide mass fingerprinting.

L15 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 1999:432183 BIOSIS
DN PREV199900432183
TI A dynamic two-dimensional polyacrylamide gel electrophoresis database: The ***mycobacterial*** proteome via internet.
AU Mollenkopf, Hans-Joachim [Reprint author]; Jungblut, Peter Roman; Raupach, Baerbel; Mattow, Jens; ***Lamer, Stephanie*** ; Zimny-Arndt, Ursula; Schaible, Ulrich Emil; Kaufmann, Stefan Hugo Ernst
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Electrophoresis, (Aug., 1999) Vol. 20, No. 11, pp. 2172-2180. print.

CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB Proteome analysis by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry, in combination with protein chemical methods, is a powerful approach for the analysis of the protein composition of complex biological samples. Data organization is imperative for efficient handling of the vast amount of information generated. Thus we have constructed a 2-D PAGE database to store and compare protein patterns of cell-associated and culture-supernatant proteins of different ***mycobacterial*** strains. In accordance with the guidelines for federated 2-DE databases, we developed a program that generates a dynamic 2-D PAGE database for the World-Wide-Web to organise and publish, via the internet, our results from proteome analysis of different ***Mycobacterium*** tuberculosis as well as ***Mycobacterium*** bovis BCG strains. The uniform resource locator for the database is http://www.mpiib-berlin.mpg.de/2D-PAGE and can be read with a Java compatible browser. The interactive hypertext markup language documents displayed are generated dynamically in each individual session from a rational data file, a 2-D gel image file and a map file describing the protein spots as polygons. The program consists of common gateway interface scripts written in PERL, minimizing the administrative workload of the database. Furthermore, the database facilitates not only interactive use, but also worldwide active participation of other scientific groups with their own data, requiring only minimal computer hardware and knowledge of information technology.

L15 ANSWER 7 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 5
AN 1999:470696 BIOSIS
DN PREV199900470696
TI Comparative proteome analysis of ***Mycobacterium*** tuberculosis and ***Mycobacterium*** bovis BCG strains: Towards functional genomics of microbial pathogens.
AU Jungblut, P. R. [Reprint author]; Schaible, U. E.; Mollenkopf, H.-J.; Zimny-Arndt, U.; Raupach, B.; Mattow, J.; Halada, P.; ***Lamer, S.*** ; Hagens, K.; Kaufmann, S. H. E.
CS Protein Analysis Unit, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Molecular Microbiology, (Sept., 1999) Vol. 33, No. 6, pp. 1103-1117. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 9 Nov 1999
Last Updated on STN: 9 Nov 1999
AB In 1993, the WHO declared tuberculosis a global emergency on the basis that there are 8 million new cases per year. The complete genome of the strain H37Rv of the causative microorganism, ***Mycobacterium*** tuberculosis, comprising 3924 genes has been sequenced. We compared the proteomes of two non-virulent vaccine strains of M. bovis BCG (Chicago and Copenhagen) with two virulent strains of M. tuberculosis (H37Rv and Erdman) to identify protein candidates of value for the development of vaccines, diagnostics and therapeutics. The ***mycobacterial*** strains were analysed by two-dimensional electrophoresis (2-DE) combining non-equilibrium pH gradient electrophoresis (NEPHGE) with SDS-PAGE. Distinct and characteristic proteins were identified by mass spectrometry and introduced into a dynamic 2-DE database (http://www.mpiib-berlin.mpg.de/2D-PAGE). Silver-stained 2-DE patterns of ***mycobacterial*** cell proteins or culture supernatants contained 1800 or 800 spots, respectively, from which 263 wereidentified. Of these, 54 belong to the culture supernatant. Sixteen and 25 proteins differing in intensity or position between M. tuberculosis H37Rv and Erdman, and H37Rv and M. bovis BCG Chicago, respectively, were identified and categorized into protein classes. It is to be hoped that the availability of the ***mycobacterial*** proteome will facilitate the design of novel measures for prevention and therapy of one of the great health threats, tuberculosis.

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=> e mattow jens/au
E1          11     MATTOVA M/AU
E2          38     MATTOW J/AU
E3          30 --> MATTOW JENS/AU
E4           2     MATTOWITZ MIETKE R/AU
E5           5     MATTOWITZ R/AU
E6           1     MATTOWN J/AU
E7           7     MATTOX/AU
E8          11     MATTOX A/AU
E9           1     MATTOX A COLIN/AU
E10         13     MATTOX A J/AU
E11          4     MATTOX ADANDE/AU
E12          8     MATTOX ADANDE J/AU

=> s e2-e3 and mycobact?
L16         54 ("MATTOW J"/AU OR "MATTOW JENS"/AU) AND MYCOBACT?

=> dup rem l16
PROCESSING COMPLETED FOR L16
L17          14 DUP REM L16 (40 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 14 ANSWERS - CONTINUE? Y/(N):y

L17  ANSWER 1 OF 14  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 1
AN   2004:150099  BIOSIS
DN   PREV200400154284
TI   Complementary analysis of the  ***Mycobacterium***  tuberculosis
     proteome by two-dimensional electrophoresis and isotope-coded affinity tag
     technology.
AU   Schmidt, Frank; Donahoe, Samuel; Hagens, Kristine;  ***Mattow, Jens***  ;
     Schaible, Ulrich E.; Kaufmann, Stefan H. E.; Aebersold, Ruedi; Jungblut,
     Peter R. [Reprint Author]
CS   Core Facility Protein Analysis, Max Planck Institute for Infection
     Biology, Schumannstr. 21/22, D-10117, Berlin, Germany
     jungblut@mpiib-berlin.mpg.de
SO   Molecular & Cellular Proteomics, (January 2004) Vol. 3, No. 1, pp. 24-42.
     print.
     ISSN: 1535-9476 (ISSN print).
DT   Article
LA   English
ED   Entered STN: 17 Mar 2004
     Last Updated on STN: 17 Mar 2004
AB   Classical proteomics combined two-dimensional gel electrophoresis (2-DE)
     for the separation and quantification of proteins in a complex mixture
     with mass spectrometric identification of selected proteins.  More
     recently, the combination of liquid chromatography (LC), stable isotope
     tagging, and tandem mass spectrometry (MS/MS) has emerged as an
     alternative quantitative proteomics technology.  We have analyzed the
     proteome of  ***Mycobacterium***  tuberculosis, a major human pathogen
     comprising about 4,000 genes, by (i) 2-DE and mass spectrometry (MS) and
     by (ii) the isotope-coded affinity tag (ICAT) reagent method and MS/MS.
     The data obtained by either technology were compared with respect to their
     selectivity for certain protein types and classes and with respect to the
     accuracy of quantification.  Initial datasets of 60,000 peptide MS/MS
     spectra and 1,800 spots for the ICAT-LC/MS and 2-DE/MS methods,
     respectively, were reduced to 280 and 108 conclusively identified and
     quantified proteins, respectively.  ICAT-LC/MS showed a clear bias for
     high Mr proteins and was complemented by the 2-DE/MS method, which showed
     a preference for low Mr proteins and also identified cysteine-free
     proteins that were transparent to the ICAT-LC/MS method.  Relative
     quantification between two strains of the M. tuberculosis complex also
     revealed that the two technologies provide complementary quantitative
     information; whereas the ICAT-LC/MS method quantifies the sum of the
     protein species of one gene product, the 2-DE/MS method quantifies at the
     level of resolved protein species, including post-translationally modified
     and processed polypeptides.  Our data indicate that different proteomic
     technologies applied to the same sample provide complementary types of
     information that contribute to a more complete understanding of the
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biological system studied.

L17 ANSWER 2 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:173461 CAPLUS
DN 138:220354
TI Vaccine against ***mycobacterial*** -induced diseases comprises Rv1511 protein or its functional epitope and chimeric protein
IN Grode, Leander; Jungblut, Peter R.; Kaufmann, Stefan H. E.; ***Mattow,*** *** Jens*** ; Mollenkopf, Hans-Joachim; Schaible, Ulrich
PA Max-Planck-Gesellschaft zur Foerderung der Wissenschaften E.V., Germany
SO PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003018053	A1	20030306	WO 2002-EP9345	20020821

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI EP 2001-120194 A 20010822
AB The present invention relates to a pharmaceutical compn. comprising Rv1511 protein or nucleic acid encoding Rv1511 protein. Furthermore, the invention provides for pharmaceutical compns. comprising fusion proteins, polynucleotides, vector(s), host cell(s) or antibodies as described herein. In addn., the invention relates to recombinant (bacterial) host cells and methods for the prodn. of a vaccine. The vaccine is used for treating ***mycobacterial*** -induced diseases such as tuberculosis, tropical skin ulcer, ulceration, abscess, granulomatous skin disease, pulmonary disease, lymphadenitis, cutaneous and disseminated disease.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 3 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 2004:71856 BIOSIS
DN PREV200400073461
TI Comparative proteome analysis of culture supernatant proteins from virulent ***Mycobacterium*** tuberculosis H37Rv and attenuated M. bovis BCG Copenhagen.
AU ***Mattow, Jens*** [Reprint Author]; Schaible, Ulrich E.; Schmidt, Frank; Hagens, Kristine; Slejak, Frank; Brestrich, Gordon; Haeselbarth, Gisela; Mueller, Eva-Christina; Jungblut, Peter R.; Kaufmann, Stefan H. E.
CS Department of Immunology, Max Planck Institute for Infection Biology, Schumannstr. 21-22, D-10117, Berlin, Germany
mattow@mpiib-berlin.mpg.de
SO Electrophoresis, (October 2003) Vol. 24, No. 19-20, pp. 3405-3420. print.
ISSN: 0173-0835 (ISSN print).
DT Article
LA English
ED Entered STN: 4 Feb 2004
Last Updated on STN: 4 Feb 2004
AB A comprehensive analysis of culture supernatant (CSN) proteins of ***Mycobacterium*** tuberculosis H37Rv was accomplished by combination of two-dimensional electrophoresis (2-DE), mass spectrometry, and N-terminal sequencing by Edman degradation. Analytical 2-DE gels resolved approximately 1250 protein spots from CSN of M. tuberculosis H37Rv, 381 of which were identified by mass spectrometry and/or Edman degradation. This study revealed 137 different proteins, 42 of which had previously been described as secreted. Comparative proteome analysis of CSN from virulent M. tuberculosis H37Rv and attenuated ***Mycobacterium*** bovis BCG Copenhagen identified 39 M. tuberculosis-specific spots containing 27

different proteins, representing candidate antigens for novel vaccines and diagnostics in tuberculosis. These included five proteins encoded by open reading frames absent from M. bovis BCG, e.g., early secretory antigen target (Esat6), as well as 22 novel differential proteins, such as acetyl-CoA C-acetyltransferase (Rv0243) and two putative Esat6-like proteins (Rv1198, Rv1793).

L17 ANSWER 4 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 2004:71349 BIOSIS
DN PREV200400073000
TI The RD1 proteins of ***Mycobacterium*** tuberculosis: Expression in ***Mycobacterium*** smegmatis and biochemical characterization.
AU Daugelat, Sabine [Reprint Author]; Kowall, Jane; ***Mattow, Jens*** ; Bumann, Dirk; Winter, Ralf; Hurwitz, Robert; Kaufmann, Stefan H. E.
CS Novartis Institute for Tropical Diseases Pte Ltd., 1 Science Park Road, Singapore Science Park II, No. 04-14 The Capricorn, Singapore, 117528, Singapore
sabine.daugelat@group.novartis.com
SO Microbes and Infection, (October 2003) Vol. 5, No. 12, pp. 1082-1095. print.
ISSN: 1286-4579.
DT Article
LA English
ED Entered STN: 4 Feb 2004
Last Updated on STN: 4 Feb 2004
AB A 9.5-kb section of DNA called region of deletion 1 (RD1) is present in virulent ***Mycobacterium*** tuberculosis strains but is deleted in all attenuated ***Mycobacterium*** bovis BCG vaccine strains. This region codes for at least nine genes. Some or all RD1 gene products may be involved in virulence and pathogenesis, and at least two, ESAT-6 and CFP-10, represent potent T- and B-cell antigens. In order to produce the entire set of RD1 proteins with their natural posttranslational modifications, a robust expression system for M. tuberculosis proteins in the fast-growing saprophytic strain ***Mycobacterium*** smegmatis was developed. Our system employs the inducible acetamidase promoter and allows translational fusion of recombinant M. tuberculosis proteins with polyhistidine or influenza hemagglutinin epitope tags for affinity purification. Using eGFP as reporter gene, we showed that the acetamidase promoter is tightly regulated in M. smegmatis and that this promoter is much stronger than the widely used constitutive groEL2 promoter. We then cloned 11 open reading frames (ORFs) found within RD1 and successfully expressed and purified the respective proteins. Sera from tuberculosis patients and M. tuberculosis-infected mice reacted with 10 purified RD1 proteins, thus demonstrating that Rv3871, Rv3872, Rv3873, CFP-10, ESAT-6, Rv3876, Rv3878, Rv3879c and ORF-14 are expressed in vivo. Finally, glycosylation of the RD1 proteins was analyzed. We present preliminary evidence that the PPE protein Rv3873 is glycosylated at its C terminus, thus highlighting the ability of M. smegmatis to produce M. tuberculosis proteins bearing posttranslational modifications.

L17 ANSWER 5 OF 14 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2003:785301 SCISEARCH
GA The Genuine Article (R) Number: 718AW
TI Iterative data analysis is the key for exhaustive analysis of peptide mass fingerprints from proteins separated by two-dimensional electrophoresis
AU Schmidt F; Schmid M; Jungblut P R (Reprint); ***Mattow J*** ; Facius A; Pleissner K P
CS Max Planck Inst Infect Biol, Core Facil Protein Anal, Schumannstr 21-22, D-10117 Berlin, Germany (Reprint); Max Planck Inst Infect Biol, Core Facil Protein Anal, D-10117 Berlin, Germany; Max Planck Inst Infect Biol, Dept Immunol, Berlin, Germany; GSF, Ctr Environm & Hlth, Inst Bioinformat, Berlin, Germany; Max Planck Inst Infect Biol, Core Facil Bioinformat, D-10117 Berlin, Germany
CYA Germany
SO JOURNAL OF THE AMERICAN SOCIETY FOR MASS SPECTROMETRY, (SEP 2003) Vol. 14, No. 9, pp. 943-956.
Publisher: ELSEVIER SCIENCE INC, 360 PARK AVE SOUTH, NEW YORK, NY 10010-1710 USA.
ISSN: 1044-0305.
DT Article; Journal

LA English
REC Reference Count: 39
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Peptide mass fingerprinting (PMF) is a powerful tool for identification of proteins separated by two-dimensional electrophoresis (2-DE). With the increase in sensitivity of peptide mass determination it becomes obvious that even spots looking well separated on a 2-DE gel may consist of several proteins. As a result the number of mass peaks in PMFs increased dramatically leaving many unassigned after a first database search. A number of these are caused by experiment-specific contaminants or by neighbor spots, as well as by additional proteins or post-translational modifications. To understand the complete protein composition of a spot we suggest an iterative procedure based on large numbers of PMFs, exemplified by PMFs of 480 Helicobacter pylori protein spots. Three key iterations were applied: (1) Elimination of contaminant mass peaks determined by MS-Screener (a software developed for this purpose) followed by reanalysis; (2) neighbor spot mass peak determination by cluster analysis, elimination from the peak list and repeated search; (3) re-evaluation of contaminant peaks. The quality of the identification was improved and spots previously unidentified were assigned to proteins. Eight additional spots were identified with this procedure, increasing the total number of identified spots to 455.

L17 ANSWER 6 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:54667 BIOSIS
DN PREV200300054667
TI Vaccine candidates by classical proteomics: Breakthrough for the development of a new vaccine against tuberculosis?.
AU Jungblut, P. R. [Reprint Author]; ***Mattow, J.*** [Reprint Author]; Grode, L. [Reprint Author]; Schaible, U. [Reprint Author]; Kaufmann, S. H. E. [Reprint Author]
CS Department Immunology, Max Planck Institute for Infection Biology, D-10117, Berlin, Germany
SO Molecular & Cellular Proteomics, (September 2002) Vol. 1, No. 9, pp. 704. print.
Meeting Info.: First World Congress of the Human Proteome Organisation. Versailles, Paris, France. November 21-24, 2002. Human Proteome Organisation.
ISSN: 1535-9476 (ISSN print).
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 22 Jan 2003
Last Updated on STN: 22 Jan 2003

L17 ANSWER 7 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
AN 2003:101214 CAPLUS
DN 139:288488
TI ***Mycobacterial*** proteomes
AU Mollenkopf, Hans-Joachim; ***Mattow, Jens*** ; Schaible, Ulrich E.; Grode, Leander; Kaufmann, Stefan H. E.; Jungblut, Peter R.
CS Department of Immunology, Max Planck Institute for Infection Biology, Berlin, D-10117, Germany
SO Methods in Enzymology (2002), 358(Bacterial Pathogenesis, Part C), 242-256
CODEN: MENZAU; ISSN: 0076-6879
PB Elsevier Science
DT Journal
LA English
AB The procedures for the two-dimensional gel electrophoresis for protein sepn. in combination with mass spectrometry (MS) for the identification and characterization of gel-sepd. proteins to systematically analyze the proteomes of different virulent and attenuated strains is described. The identification of ***Mycobacterium*** tuberculosis specific proteins is potential antigens for diagnosis of and vaccination against tuberculosis.

L17 ANSWER 8 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 5
AN 2001:440783 BIOSIS
DN PREV200100440783
TI Proteomics reveals open reading frames in ***Mycobacterium***

tuberculosis H37Rv not predicted by genomics.
AU Jungblut, Peter R. [Reprint author]; Mueller, Eva-Christina; ***Mattow,*** *** Jens*** ; Kaufmann, Stefan H. E.
CS Core Facility for Protein Analysis, Max Planck Institute for Infection Biology, Schumannstr. 21-22, D-10117, Berlin, Germany jungblut@mpiib-berlin.mpg.de
SO Infection and Immunity, (September, 2001) Vol. 69, No. 9, pp. 5905-5907. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 19 Sep 2001
Last Updated on STN: 22 Feb 2002
AB Genomics revealed the sequence of 3924 genes of the H37Rv strain of ***Mycobacterium*** tuberculosis. Proteomics complements genomics in showing which genes are really expressed, and here we show the expression of six genes not predicted by genomics, as proved by two-dimensional electrophoresis and matrix-assisted laser desorption ionization and nano-electrospray mass spectrometry.

L17 ANSWER 9 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 2001:472668 BIOSIS
DN PREV200100472668
TI Identification of proteins from ***Mycobacterium*** tuberculosis missing in attenuated ***Mycobacterium*** bovis BCG strains.
AU ***Mattow, Jens*** ; Jungblut, Peter R. [Reprint author]; Schaible, Ulrich E.; Mollenkopf, Hans-Joachim; Lamer, Stephanie; Zimny-Arndt, Ursula; Hagens, Kristine; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS Central Support Unit Biochemistry, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany jungblut@mpiib-berlin.mpg.de
SO Electrophoresis, (August, 2001) Vol. 22, No. 14, pp. 2936-2946. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 10 Oct 2001
Last Updated on STN: 23 Feb 2002
AB A proteome approach, combining high-resolution two-dimensional electrophoresis (2-DE) with mass spectrometry, was used to compare the cellular protein composition of two virulent strains of ***Mycobacterium*** tuberculosis with two attenuated strains of ***Mycobacterium*** bovis Bacillus Calmette-Guerin (BCG), in order to identify unique proteins of these strains. Emphasis was given to the identification of M. tuberculosis specific proteins, because we consider these proteins to represent putative virulence factors and interesting candidates for vaccination and diagnosis of tuberculosis. The genome of M. tuberculosis strain H37Rv comprises nearly 4000 predicted open reading frames. In contrast, the separation of proteins from whole ***mycobacterial*** cells by 2-DE resulted in silver-stained patterns comprising about 1800 distinct protein spots. Amongst these, 96 spots were exclusively detected either in the virulent (56 spots) or in the attenuated (40 spots) ***mycobacterial*** strains. Fifty-three of these spots were analyzed by mass spectrometry, of which 41 were identified, including 32 M. tuberculosis specific spots. Twelve M. tuberculosis specific spots were identified as proteins, encoded by genes previously reported to be deleted in M. bovis BCG. The remaining 20 spots unique for M. tuberculosis were identified as proteins encoded by genes that are not known to be missing in M. bovis BCG.

L17 ANSWER 10 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7
AN 2001:378769 BIOSIS
DN PREV200100378769
TI Identification of acidic, low molecular mass proteins of ***Mycobacterium*** tuberculosis strain H37Rv by matrix-assisted laser desorption/ionization and electrospray ionization mass spectrometry.
AU ***Mattow, Jens*** [Reprint author]; Jungblut, Peter R.; Mueller, Eva-Christina; Kaufmann, Stefan H. E.
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Schumannstr. 21/22, D-10117, Berlin, Germany

mattow@mpiib-berlin.mpg.de
SO Proteomics, (April, 2001) Vol. 1, No. 4, pp. 494-507. print.
ISSN: 1615-9853.
DT Article
LA English
ED Entered STN: 8 Aug 2001
Last Updated on STN: 19 Feb 2002
AB Matrix-assisted laser desorption/ionization-mass spectrometry peptide mass mapping and nano-electrospray ionization tandem mass spectrometry were used to identify acidic, low molecular mass proteins of ***Mycobacterium*** tuberculosis strain H37Rv. Proteins were extracted from whole cell lysates of ***mycobacteria*** , separated by high resolution two-dimensional electrophoresis (2-DE) and analysed by mass spectrometry (MS). Silver-stained 2-DE patterns resolved about 1800 distinct protein species, 190 of which had an observed isoelectric point and molecular mass in the range of pH 4 to 6 and 6 to 15 kDa, respectively. Seventy-six spots from this range were excised from Coomassie Brilliant Blue G250-stained gels and analysed by MS, from which 72 were identified. These spots were shown to represent products of as many as 50 different protein-coding genes. Ten genes gave rise to more than one protein species. Eleven spots contained more than one protein. The present study led to the identification of 15 ***mycobacterial*** proteins with assigned putative functions, 28 conserved hypothetical proteins and one unknown protein. Most proteins of the latter two groups had previously been predicted at the DNA level only. Six additional spots were shown to comprise proteins encoded by open reading frames that have not been predicted for M. tuberculosis H37Rv by genomic investigations.

L17 ANSWER 11 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS
DN 133:149124
TI Identification of specific differentially expressed antigens
IN Jungblut, Peter; Kaufmann, Stefan H. E.; Schaible, Ulrich; Mollenkopf, Hans; Raupach, Barbel; Zimny-Arndt, Ursula; Lamer, Stephanie; ***Mattow,*** *** Jens***
PA Chiron Behring G.m.b.H. und Co., Germany
SO PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000044392	A2	20000803	WO 2000-EP690	20000128
	WO 2000044392	A3	20001207		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1146889	A2	20011024	EP 2000-904979	20000128
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2002534994	T2	20021022	JP 2000-595694	20000128
PRAI	EP 1999-101590	A	19990129		
	WO 2000-EP690	W	20000128		

AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is differentially expressed in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for

the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

L17 ANSWER 12 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8
AN 2000:227162 BIOSIS
DN PREV200000227162
TI Analysis of missed cleavage sites, tryptophan oxidation and N-terminal pyroglutamylation after in-gel tryptic digestion.
AU Thiede, Bernd [Reprint author]; Lamer, Stephanie; ***Mattow, Jens*** ; Siejak, Frank; Dimmler, Christiane; Rudel, Thomas; Jungblut, Peter R.
CS Max-Planck-Institut fuer Infektions-Biologie, Monbijoustrasse 2, D-10117, Berlin, Germany
SO Rapid Communications in Mass Spectrometry, (2000) Vol. 14, No. 6, pp. 496-502. print.
CODEN: RCMSEF. ISSN: 0951-4198.
DT Article
LA English
ED Entered STN: 7 Jun 2000
Last Updated on STN: 5 Jan 2002
AB Peptide mass fingerprinting is a powerful tool for the identification of proteins. Trypsin is the most widely used enzyme for this purpose. Therefore, 104 protein digests from human Jurkat T cells and ***Mycobacterium*** were analyzed considering missed cleavage sites, tryptophan oxidation and N-terminal pyroglutamylation. About 90% of the matched peptides with missed cleavage sites could be classified into three groups: (i) lysine and arginine with a neighbouring proline on the carboxy-terminal side, (ii) neighboring lysines/arginines, and (iii) lysines and arginines with an aspartic acid or glutamic acid residue on either the amino- or carboxy-terminal side. The first group is already accounted for by search programs. The number of missed cleavage sites can be increased without reducing the precision of the database search by taking the other two groups into consideration. Peptides with tryptophan were observed in non, singly (+16 Da) and doubly (+32 Da) oxidized forms. The higher oxidized form was only observed with lower intensity in the presence of the lower oxidized form. Peptides with N-terminal glutamine were found always as pyroglutamate (-17 Da), and in the majority of cases in pairs with unmodified glutamine. These data can be used for the refinement of protein searches by peptide mass fingerprinting.

L17 ANSWER 13 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 1999:432183 BIOSIS
DN PREV199900432183
TI A dynamic two-dimensional polyacrylamide gel electrophoresis database: The ***mycobacterial*** proteome via internet.
AU Mollenkopf, Hans-Joachim [Reprint author]; Jungblut, Peter Roman; Raupach, Baerbel; ***Mattow, Jens*** ; Lamer, Stephanie; Zimny-Arndt, Ursula; Schaible, Ulrich Emil; Kaufmann, Stefan Hugo Ernst
CS Department of Immunology, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Electrophoresis, (Aug., 1999) Vol. 20, No. 11, pp. 2172-2180. print.
CODEN: ELCTDN. ISSN: 0173-0835.
DT Article
LA English
ED Entered STN: 18 Oct 1999
Last Updated on STN: 18 Oct 1999
AB Proteome analysis by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry, in combination with protein chemical methods, is a powerful approach for the analysis of the protein composition of complex biological samples. Data organization is imperative for efficient handling of the vast amount of information generated. Thus we have constructed a 2-D PAGE database to store and compare protein patterns of cell-associated and culture-supernatant proteins of different ***mycobacterial*** strains. In accordance with the guidelines for federated 2-DE databases, we developed a program that generates a dynamic 2-D PAGE database for the World-Wide-Web to organise and publish, via the internet, our results from proteome analysis of different ***Mycobacterium*** tuberculosis as well as ***Mycobacterium*** bovis BCG strains. The uniform resource locator for

the database is http://www.mpiib-berlin.mpg.de/2D-PAGE and can be read with a Java compatible browser. The interactive hypertext markup language documents displayed are generated dynamically in each individual session from a rational data file, a 2-D gel image file and a map file describing the protein spots as polygons. The program consists of common gateway interface scripts written in PERL, minimizing the administrative workload of the database. Furthermore, the database facilitates not only interactive use, but also worldwide active participation of other scientific groups with their own data, requiring only minimal computer hardware and knowledge of information technology.

L17 ANSWER 14 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10
AN 1999:470696 BIOSIS
DN PREV199900470696
TI Comparative proteome analysis of ***Mycobacterium*** tuberculosis and ***Mycobacterium*** bovis BCG strains: Towards functional genomics of microbial pathogens.
AU Jungblut, P. R. [Reprint author]; Schaible, U. E.; Mollenkopf, H.-J.; Zimny-Arndt, U.; Raupach, B.; ***Mattow, J.*** ; Halada, P.; Lamer, S.; Hagens, K.; Kaufmann, S. H. E.
CS Protein Analysis Unit, Max-Planck-Institute for Infection Biology, Monbijoustr. 2, D-10117, Berlin, Germany
SO Molecular Microbiology, (Sept., 1999) Vol. 33, No. 6, pp. 1103-1117. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 9 Nov 1999
Last Updated on STN: 9 Nov 1999
AB In 1993, the WHO declared tuberculosis a global emergency on the basis that there are 8 million new cases per year. The complete genome of the strain H37Rv of the causative microorganism, ***Mycobacterium*** tuberculosis, comprising 3924 genes has been sequenced. We compared the proteomes of two non-virulent vaccine strains of M. bovis BCG (Chicago and Copenhagen) with two virulent strains of M. tuberculosis (H37Rv and Erdman) to identify protein candidates of value for the development of vaccines, diagnostics and therapeutics. The ***mycobacterial*** strains were analysed by two-dimensional electrophoresis (2-DE) combining non-equilibrium pH gradient electrophoresis (NEPHGE) with SDS-PAGE. Distinct and characteristic proteins were identified by mass spectrometry and introduced into a dynamic 2-DE database (http://www.mpiib-berlin.mpg.de/2D-PAGE). Silver-stained 2-DE patterns of ***mycobacterial*** cell proteins or culture supernatants contained 1800 or 800 spots, respectively, from which 263 wereidentified. Of these, 54 belong to the culture supernatant. Sixteen and 25 proteins differing in intensity or position between M. tuberculosis H37Rv and Erdman, and H37Rv and M. bovis BCG Chicago, respectively, were identified and categorized into protein classes. It is to be hoped that the availability of the ***mycobacterial*** proteome will facilitate the design of novel measures for prevention and therapy of one of the great health threats, tuberculosis.

=> s mycobact? and (differential? express?)
3 FILES SEARCHED...
L18 1815 MYCOBACT? AND (DIFFERENTIAL? EXPRESS?)

=> dup rem l18
PROCESSING IS APPROXIMATELY 86% COMPLETE FOR L18
PROCESSING COMPLETED FOR L18
L19 1455 DUP REM L18 (360 DUPLICATES REMOVED)

=> s l19 and ((isopropyl malate synthase)or(Rv3710))
L20 1 L19 AND ((ISOPROPYL MALATE SYNTHASE) OR(RV3710))

=> d bib ab

L20 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:535006 CAPLUS
DN 133:149124

```
TI   Identification of specific   ***differentially***     ***expressed***
     antigens
IN   Jungblut, Peter; Kaufmann, Stefan H. E.; Schaible, Ulrich; Mollenkopf,
     Hans; Raupach, Barbel; Zimny-Arndt, Ursula; Lamer, Stephanie; Mattow, Jens
PA   Chiron Behring G.m.b.H. und Co., Germany
SO   PCT Int. Appl., 110 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   WO 2000044392     A2    20000803       WO 2000-EP690    20000128
     WO 2000044392     A3    20001207
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
             CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
             IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
             MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
             SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
             AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
             DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
             CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     EP 1146889        A2    20011024       EP 2000-904979   20000128
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO
     JP 2002534994     T2    20021022       JP 2000-595694   20000128
PRAI EP 1999-101590    A     19990129
     WO 2000-EP690     W     20000128
AB   The present invention relates to compns. useful in immunization against
     pathogenic organisms of the genus   ***Mycobacterium***   and for
     diagnostic purposes.  In particular, the present invention relates to a
     compn. comprising at least one protein which is   ***differentially***
       ***expressed***   in a virulent strain as compared to an avirulent strain
     of   ***Mycobacteria***   .  Furthermore, the invention relates to compns.
     comprising fusion proteins, antigenic fragments, nucleic acid mols.
     encoding the aforementioned proteinaceous compds. and/or antibodies
     thereto.  Addnl., the invention relates to pharmaceutical and diagnostic
     compns. comprising or employing compds. of the invention.  In addn., the
     present invention relates to the use of the compds. of the invention for
     the treatment of   ***Mycobacterium***   induced diseases and/or for the
     prepn. of a vaccine for vaccination against   ***Mycobacterium***
     induced diseases.


=> s l19 and ((s-adenosylmethionine synthase metK)or(Rv1392))
L21          1 L19 AND ((S-ADENOSYLMETHIONINE SYNTHASE METK) OR(RV1392))

=> d bib ab

L21  ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2000:535006  CAPLUS
DN   133:149124
TI   Identification of specific   ***differentially***     ***expressed***
     antigens
IN   Jungblut, Peter; Kaufmann, Stefan H. E.; Schaible, Ulrich; Mollenkopf,
     Hans; Raupach, Barbel; Zimny-Arndt, Ursula; Lamer, Stephanie; Mattow, Jens
PA   Chiron Behring G.m.b.H. und Co., Germany
SO   PCT Int. Appl., 110 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   WO 2000044392     A2    20000803       WO 2000-EP690    20000128
     WO 2000044392     A3    20001207
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
             CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
             IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
             MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
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SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1146889 A2 20011024 EP 2000-904979 20000128
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO
JP 2002534994 T2 20021022 JP 2000-595694 20000128
PRAI EP 1999-101590 A 19990129
WO 2000-EP690 W 20000128
AB The present invention relates to compns. useful in immunization against pathogenic organisms of the genus ***Mycobacterium*** and for diagnostic purposes. In particular, the present invention relates to a compn. comprising at least one protein which is ***differentially*** ***expressed*** in a virulent strain as compared to an avirulent strain of ***Mycobacteria*** . Furthermore, the invention relates to compns. comprising fusion proteins, antigenic fragments, nucleic acid mols. encoding the aforementioned proteinaceous compds. and/or antibodies thereto. Addnl., the invention relates to pharmaceutical and diagnostic compns. comprising or employing compds. of the invention. In addn., the present invention relates to the use of the compds. of the invention for the treatment of ***Mycobacterium*** induced diseases and/or for the prepn. of a vaccine for vaccination against ***Mycobacterium*** induced diseases.

=> s l19 and ((succinyl-coa synthase)or(Rv0952))
L22 0 L19 AND ((SUCCINYL-COA SYNTHASE) OR(RV0952))